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Sequence Listing

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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
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Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
170 175 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
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Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
215 220 225

Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
230 235 240

Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
245 250 255

Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
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Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
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Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
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<213> Homo sapiens

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 <211> 699
 <212> PRT
 <213> Homo sapiens

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 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

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100-443887-100

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Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys		
	605		610		615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe		
	620		625		630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln		
	635		640		645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe		
	650		655		660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp		
	665		670		675
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<210> 13
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 14
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 14
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<220>
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<400> 15

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<211> 1524

<212> DNA

<213> Homo sapiens

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 <211> 327
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 <213> Homo sapiens

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 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25, 65-71, 247-253, 285-291, 303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

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 35 40 45

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<211> 23
<212> DNA
<<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
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<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
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<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

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<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

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<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18
<223> Growth factor and cytokines receptors family.

<400> 22
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65 70

<210> 23
<211> 2883
<212> DNA
<213> Homo sapiens

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 <211> 616
 <212> PRT
 <213> Homo sapiens

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 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

(The following information was obtained from the records of the Federal Bureau of Investigation, Department of Justice.)

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				35					40				45
Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala
				50					55				60
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu
				65					70				75
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser
				80					85				90
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Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser
				110					115				120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu
				125					130				135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe
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				185					190				195
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Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro
				215					220				225
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu
				230					235				240
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SUBJECT:

SECRET

Ser

<220>
<223> Synthetic oligonucleotide probe

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<212> DNA
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<220>
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<220>
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<213> Homo sapiens
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<210> 29

<211> 81

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

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<221> sig_peptide
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<223> Signal peptide.

<400> 29

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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45

Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
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Lys Gly Ser Gln Lys Ser
80

<210> 30

<211> 2128

<212> DNA

<213> Homo sapiens

[The page contains several lines of extremely faint, illegible text, likely bleed-through from the reverse side.]

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 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr	110	115	120
Pro Thr Thr Tyr	Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp	125	130	135
His Ala Ile Ala	Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala	140	145	150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile	155	160	165
Thr Gly Tyr Met	Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu	170	175	180
Thr Phe Val Ala	Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn	185	190	195
Leu Tyr Gln His	Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr	200	205	210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu	215	220	225
Gly Glu Cys Thr	Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu	230	235	240
Ser Gly Leu Ala	Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu	245	250	255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln	260	265	270
Pro Arg Arg Ser	Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr	275	280	285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr	290	295	300
Ala Ile Asn Leu	Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala	305	310	315
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SECRET

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<213> Homo sapiens

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Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
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His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
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Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
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Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
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Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
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Glu Pro Glu Glu Gln
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Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135

Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150

Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165

Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180

Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
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Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
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Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
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Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
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275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
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<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu	35	40	45	
Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu	50	55	60	
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr	65	70	75	
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys	80	85	90	
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu	95	100	105	
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp	110	115	120	
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp	125	130	135	
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr	140	145	150	
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu	155	160	165	
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe	170	175	180	
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val	185	190	195	
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn	200	205	210	
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe	215	220	225	
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala				

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 <213> Artificial Sequence

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<210> 47
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<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250

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[illegible]

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Phe	Leu	Leu	Met	Phe 110	Ile	Val	Cys	Ala	Ala 115	Val	Ile	Thr	Arg	Gln 120
Lys	Gln	Lys	Ala	Ser 125	Ala	Tyr	Tyr	Pro	Ser 130	Ser	Phe	Pro	Lys	Lys 135
Lys	Tyr	Val	Asp	Gln 140	Ser	Asp	Arg	Ala	Gly 145	Gly	Pro	Arg	Ala	Phe 150
Ser	Glu	Val	Pro	Asp 155	Arg	Ala	Pro	Asp	Ser 160	Arg	Pro	Glu	Glu	Ala 165
Leu	Asp	Ser	Ser	Arg 170	Gln	Leu	Gln	Ala	Asp 175	Ile	Leu	Ala	Ala	Thr 180
Gln	Asn	Leu	Lys	Ser 185	Pro	Thr	Arg	Ala	Ala 190	Leu	Gly	Gly	Gly	Asp 195
Gly	Ala	Arg	Met	Val 200	Glu	Gly	Arg	Gly	Ala 205	Glu	Glu	Glu	Glu	Lys 210
Gly	Ser	Gln	Glu	Gly 215	Asp	Gln	Glu	Val	Gln 220	Gly	His	Gly	Val	Pro 225
Val	Glu	Thr	Pro	Glu 230	Ala	Gln	Glu	Glu	Pro 235	Cys	Ser	Gly	Val	Leu 240
Glu	Gly	Ala	Val	Val 245	Ala	Gly	Glu	Gly	Gln 250	Gly	Glu	Leu	Glu	Gly 255
Ser	Leu	Leu	Leu	Ala 260	Gln	Glu	Ala	Gln	Gly 265	Pro	Val	Gly	Pro	Pro 270
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cctggcctgc ctctgctgg cctctgcct gggcagtgga gaggctggcc 250
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SECRET

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

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20 25 30

Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
35 40 45

Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly
50 55 60

Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr
65 70 75

Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly
80 85 90

Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala
95 100 105

Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val
110 115 120

Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
125 130 135

Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
140 145 150

Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
155 160 165

Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
170 175 180

Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
185 190 195

Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
200 205 210

Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
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(Faint bleed-through from the reverse side of the page)

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<212> DNA
<213> Homo sapiens
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<210> 54

<211> 280

<212> PRT

<213> Homo sapiens

<400> 54

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				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
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Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
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Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
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<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg	35	40	45	
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro	50	55	60	
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Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro	80	85	90	
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	95	100	105	
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Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln	125	130	135	
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Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val	155	160	165	
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His Val Tyr Gly Met Val Pro Pro Asn	Tyr Cys Ser Gln Arg	Pro
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Arg Leu Gln Arg Met Pro Tyr His Tyr	Tyr Glu Pro Lys Gly	Pro
245	250	255
Asp Glu Cys Val Thr Tyr Ile Gln Asn	Glu His Ser Arg Lys	Gly
260	265	270
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 <211> 1115
 <212> PRT
 <213> Homo sapiens

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 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
 35 40 45
 Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
 50 55 60
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
 65 70 75
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
 80 85 90

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln
95 100 105

Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala
110 115 120

Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln
125 130 135

His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys
140 145 150

His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val
155 160 165

Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met
170 175 180

Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu
185 190 195

Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val
200 205 210

Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr
215 220 225

Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile
230 235 240

Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser
245 250 255

Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser
260 265 270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
275 280 285

Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met
290 295 300

Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr
305 310 315

Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
320 325 330

Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
335 340 345

Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
350 355 360

Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
365 370 375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
 395 400 405
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
 410 415 420
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
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 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
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 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg
 560 565 570
 Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln
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 Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp
 590 595 600
 His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile
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 Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg
 620 625 630
 Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys
 635 640 645
 Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile
 650 655 660

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<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63
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 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg
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 35 40 45
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

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Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser
				80					85					90
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg
				95					100					105
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe
				110					115					120
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val
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Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp
				140					145					150
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His
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Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala
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Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val
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Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser
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Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys
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Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met
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Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
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Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala
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Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro
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Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu
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Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly
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Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu
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Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg
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Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp
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Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
365 370 375

Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu
380 385 390

Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
395 400 405

Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val
410 415 420

Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser
425 430 435

His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val
440 445 450

Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala
455 460 465

Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro
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Thr Phe Thr Gln Trp Leu Cys
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 64
ccttcacctg cagtacacca tgggc 25

<210> 65
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
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 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 80 85 90
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 95 100 105
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 110 115 120
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 125 130 135
 Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
 155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180

Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

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Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn					
	305		310		315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr					
	320		325		330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg					
	335		340		345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp					
	350		355		360
Leu Ile Arg					

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<220>
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<400> 73
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<210> 74
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 <212> DNA
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<220>
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<400> 74
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<210> 75
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<210> 76
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 <212> DNA
 <213> Homo sapiens

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 155 160 165
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 170 175 180
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
 185 190 195
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
 200 205 210
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
 215 220 225
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
 230 235 240
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
 245 250 255
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu
 260 265 270
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
 275 280 285
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150

cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

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 ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350
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 cccaagatgc cagtgaagca cgtccatgcc catccgtgc aaggcagata 1650

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Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe
				155					160					165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr
				170					175					180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met
				185					190					195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr
				200					205					210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp
				215					220					225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe
				230					235					240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu
				245					250					255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe
				260					265					270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser
				275					280					285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro
				290					295					300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val
				305					310					315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile
				320					325					330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe
				335					340					345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu
				350					355					360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn
				365					370					375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile
				380					385					390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys
				395					400					405
Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser
				410					415					420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
425 430 435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
440 445 450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser
455 460 465
Ala Cys Ser Thr Leu Leu Val His Leu Ile
470 475

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<220>
<223> Synthetic oligonucleotide probe

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<210> 81
<211> 23
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 81
cgtaggtgac acagaagccc agg 23

<210> 82
<211> 49
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 82
tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
<211> 1844
<212> DNA
<213> Homo sapiens

<400> 83
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Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His	620	625	630
Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp	635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly	650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile	665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr	680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser	695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly	710	715	720
Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu	725	730	735
His Ile Gln Asp			

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 <212> DNA
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu	110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	125	130	135
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390

14-00000

<210> 89

<211> 25

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
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<210> 90
<211> 22
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<213> Artificial Sequence

<220>
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<400> 90
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<210> 91
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 91
  cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
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<210> 93
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
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<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
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 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210

Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225

Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val
230 235 240

Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu
245 250 255

Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly
260 265 270

His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg
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Leu Ser Val Gly His Gln His
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<211> 25
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<210> 97
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 97
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<210> 98
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 98
ggatgatttc atctccatta gcctgctgct tctggctatg ttggtgggat 50

<210> 99
<211> 1429

Figure 1 consists of 12 line drawings of a chick embryo at different stages of development. The drawings are arranged in two rows of six. The top row shows the embryo at 1, 2, 3, 4, 5, and 6 days. The bottom row shows the embryo at 7, 8, 9, 10, 11, and 12 days. The drawings illustrate the progression of the embryo, from a single cell to a fully formed chick with a beak and legs.

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<400> 99
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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgetggccgc cctggtggcc tgcattcatc tcttgggctt 200
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<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg	35	40	45	
Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg	50	55	60	
Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu	65	70	75	
Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe	80	85	90	
Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val	95	100	105	
Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu	110	115	120	
Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln	125	130	135	
Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg	140	145	150	
Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu	155	160	165	
Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys	170	175	180	
Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp	185	190	195	
Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu	200	205	210	
Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly	215	220	225	
Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser				

230	235	240
Glu Val Val Leu Asp Ser Lys Arg Gln	Val Glu Lys Glu Glu Thr	
245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu	Pro Gln Arg Asp Arg Leu	
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val	Val Glu Asp Arg Pro Val	
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly	Glu Leu Gly Gln Thr Pro	
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser	Gln Glu Asn Pro Glu Met	
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln Glu	
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly	Arg Asn Gln Gln Lys Leu	
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Arg Gly Glu Asp Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu Ser	
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn Ile	
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys	Arg Asp Thr Ile Asn Leu	
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 <211> 3671
 <212> DNA
 <213> Homo sapiens

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 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
 ttttcgctgg ttgtgttggt gctgatagat gctctgcat ttgacttcgc 250
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gctttggtga tgagagtgga tgggtgctgt agctcctggt tcaggcagct 3250

Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly
 200 205 210
 Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp
 215 220 225
 Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys
 230 235 240
 His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met
 245 250 255
 Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr
 260 265 270
 Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp
 275 280 285
 His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu
 290 295 300
 Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro
 305 310 315
 Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu
 320 325 330
 Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala
 335 340 345
 Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala
 350 355 360
 Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser
 365 370 375
 Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala
 380 385 390
 Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala
 395 400 405
 Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr
 410 415 420
 Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala
 425 430 435
 Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg
 440 445 450

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu	980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010	1015	1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg
1025 1030 1035

Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe
1040 1045 1050

Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly
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Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe
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Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

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<211> 1743
<212> DNA
<213> Homo sapiens

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gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
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gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
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aatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
<211> 442
<212> PRT
<213> Homo sapiens

<400> 104
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Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
35 40 45
Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
50 55 60
Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
65 70 75
Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
80 85 90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile
				170					175					180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys
				185					190					195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys
				200					205					210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val
				215					220					225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro
				230					235					240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu
				245					250					255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser
				260					265					270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys
				275					280					285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys
				290					295					300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser
				305					310					315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu
				320					325					330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp
				335					340					345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro
				350					355					360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr
				365					370					375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
425 430 435

Leu Tyr Val Gln Met Glu Asn
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<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

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<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgccca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 109
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<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

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ggttcggcgg agcagtcacc agccggccc cctgcctggg accaccaggc 900

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Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg					
	215		220		225
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly					
	230		235		240
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val					
	245		250		255
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly					
	260		265		270
Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala					
	275		280		

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 112
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<210> 113
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 113
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<210> 114
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 114
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<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
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gtcctctctg	agccttggtt	tcttcagcag	tgagatgctc	agaataactg	1550
ctgtctccca	tgatggtgtg	gtacagcgag	ctgttgctctg	gctatggcat	1600
ggctgtgccg	ggggtgtttg	ctgagggctt	cctgtgccag	agcccagcca	1650
gagagcaggt	gcaggtgtca	tcccagagttc	aggctctgca	cggcatggag	1700
tgggaacccc	accagctgct	gctacaggac	ctgggattgc	ctgggactcc	1750
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gctcattt	1808				

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<210> 116
<211> 331
<212> PRT
<213> Homo sapiens
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Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala
1				5					10					15
Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys
				20					25					30
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly
				35					40					45
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg
				50					55					60
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys
				65					70					75
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His
				80					85					90
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg
				95					100					105
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile
				110					115					120
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr
				125					130					135
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His
				140					145					150
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala
				155					160					165
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly
				170					175					180

His	Ile	Asp	Phe	Asp 185	Asp	Leu	Asn	Trp	Gln 190	Thr	Arg	Lys	Tyr	Asn 195
Thr	Lys	Ala	Ala	Tyr 200	Cys	Gln	Ser	Lys	Leu 205	Ala	Ile	Val	Leu	Phe 210
Thr	Lys	Glu	Leu	Ser 215	Arg	Arg	Leu	Gln	Gly 220	Ser	Gly	Val	Thr	Val 225
Asn	Ala	Leu	His	Pro 230	Gly	Val	Ala	Arg	Thr 235	Glu	Leu	Gly	Arg	His 240
Thr	Gly	Ile	His	Gly 245	Ser	Thr	Phe	Ser	Ser 250	Thr	Thr	Leu	Gly	Pro 255
Ile	Phe	Trp	Leu	Leu 260	Val	Lys	Ser	Pro	Glu 265	Leu	Ala	Ala	Gln	Pro 270
Ser	Thr	Tyr	Leu	Ala 275	Val	Ala	Glu	Glu	Leu 280	Ala	Asp	Val	Ser	Gly 285
Lys	Tyr	Phe	Asp	Gly 290	Leu	Lys	Gln	Lys	Ala 295	Pro	Ala	Pro	Glu	Ala 300
Glu	Asp	Glu	Glu	Val 305	Ala	Arg	Arg	Leu	Trp 310	Ala	Glu	Ser	Ala	Arg 315
Leu	Val	Gly	Leu	Glu 320	Ala	Pro	Ser	Val	Arg 325	Glu	Gln	Pro	Leu	Pro 330

Arg

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<210> 117
<211> 2249
<212> DNA
<213> Homo sapiens
```

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<400> 117
gaagttcgcg agcgcctggca tgtggtcctg gggcgcggtt ggcggcgctg 50
ctggcgggtgc tggcgctcgg gacaggagac ccagaaaggg ctgctggctcg 100
gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200
cggtctcggg acctgactag attctacgac aaggtacttt ctttgcatga 250
ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
gagaacatcc gagctctgaa ggatggctat gagaaggctg agcaagacct 400
tccagccttt gaggaccttg agggagcagc aagggccctg atgctggctgc 450
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aggacgtgta	catgctcaat	gtgaaaggcc	tggccccgagg	tgtctttcag	500
agagtcactg	gctctgccat	cactgacctg	tacagcccca	aacggctctt	550
ttctctcaca	ggggatgact	gcttccaagt	tggcaagggtg	gcctatgaca	600
tggggggatta	ttaccatgcc	attccatggc	tggaggagggc	tgtcagttctc	650
ttccgaggat	cttacggaga	gtggaagaca	gaggatgagg	caagtctaga	700
agatgccttg	gatcacttgg	cctttgctta	tttccgggca	ggaaatgttt	750
cgtgtgccct	cagcctctct	cgggagtttc	ttctctacag	cccagataat	800
aagaggatgg	ccaggaatgt	cttgaaatat	gaaaggctct	tggcagagag	850
ccccaaccac	gtggtagctg	aggctgtcat	ccagaggccc	aatatacccc	900
acctgcagac	cagagacacc	tacgaggggc	tatgtcagac	cctgggttcc	950
cagcccactc	tctaccagat	ccctagcctc	tactgttcct	atgagaccaa	1000
ttccaacgcc	tacctgtctg	tccagcccat	ccggaaggag	gtcatccacc	1050
tggagcccta	cattgctctc	taccatgact	tcgtcagtga	ctcagaggct	1100
cagaaaatta	gagaacttgc	agaaccatgg	ctacagaggt	cagtgggtggc	1150
atcaggggag	aagcagttac	aagtggagta	ccgcatcagc	aaaagtgcct	1200
ggctgaagga	cactgttgac	ccaaaactgg	tgaccctcaa	ccaccgcatt	1250
gctgcctca	caggccttga	tgtccggcct	ccctatgcag	agtatctgca	1300
ggtggtgaac	tatggcatcg	gaggacacta	tgagcctcac	tttgaccatg	1350
ctacgtcacc	aagcagcccc	ctctacagaa	tgaagtcagg	aaaccgagtt	1400
gcaacattta	tgatctatct	gagctcggtg	gaagctggag	gagccacagc	1450
cttcatctat	gccaacctca	gcgtgcctgt	ggttaggaat	gcagcactgt	1500
tttggtggaa	cctgcacagg	agtgggtgaag	gggacagtga	cacacttcat	1550
gctggctgtc	ctgtcctggg	gggagataag	tgggtggcca	acaagtggat	1600
acatgagtat	ggacaggaat	tccgcagacc	ctgcagctcc	agccctgaag	1650
actgaactgt	tggcagagag	aagctggtgg	agtctgtgg	ctttccagag	1700
aagccaggag	ccaaaagctg	gggtaggaga	ggagaaagca	gagcagcctc	1750
ctggaagaag	gccttgctcag	ctttgtctgt	gcctcgcaaa	tcagaggcaa	1800
gggagagggt	gttaccaggg	gacactgaga	atgtacattt	gatctgcccc	1850

11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111
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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys	Phe Gln Val Gly Lys	Val Ala Tyr Asp Met	Gly
185		190	195
Asp Tyr Tyr His	Ala Ile Pro Trp Leu	Glu Glu Ala Val Ser	Leu
200		205	210
Phe Arg Gly Ser	Tyr Gly Glu Trp Lys	Thr Glu Asp Glu Ala	Ser
215		220	225
Leu Glu Asp Ala	Leu Asp His Leu Ala	Phe Ala Tyr Phe Arg	Ala
230		235	240
Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu	Leu
245		250	255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys	Tyr
260		265	270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu	Ala
275		280	285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp	Thr
290		295	300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu	Tyr
305		310	315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn	Ala
320		325	330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu	Glu
335		340	345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu	Ala
350		355	360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser	Val
365		370	375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile	Ser
380		385	390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val	Thr
395		400	405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg	Pro
410		415	420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly	Gly
425		430	435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser	Pro
440		445	450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met	Ile
455		460	465

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser
530 535 540

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122

gagataggga gtctggggtt aagtctctgc tccatctcag gagccctgc 50
 tcccacccct aggaagccac cagactccac ggtgtggggc caatcagggtg 100
 gaatcgggcc tggcagggtg ggccacgagc gctggctgag ggaccgagcc 150
 ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200
 cgcggggact cggagcagggt gcgctactgc gcgcgcttct cctacctctg 250
 gctcaagttt tcacttatca tctattccac cgtgttctg ctgattgggg 300
 ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctct 400
 gggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
 aagtgtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gccctggac cctggcctg tggggtgccc tacacctgct 750
 gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
 atcgacaagg agcgtttcag tgtgcaggat gtcactacg tgcggggctg 850
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
 gcatcctcct gggcatcctg cttccccagt tctgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
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 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
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 gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc ccagggagc 1250
 agagcctggg cctcccctaa gaggtttcc ccgaggcagc tctggaatct 1300
 gtgccacact ggggcctggg gaacaaggcc ctctttctc caggcctggg 1350
 ctacagggga gggagagcct gaggtctctg tcagggccca ttctatctct 1400

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ggggagagagg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500
gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggctgct 1600
tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650
gtacagataa caggagtttc tgactaatca aagctgggat ttccccgcatt 1700
gtcttattct tgcccttccc ccaaccagtt tgттаатcaa асааааааа 1750
catgttttgt tttgttttta aaaaaaaa 1778

$\langle 210 \rangle$ 123

<212> PRT

<400> 123

Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
20 25 30

Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
50 55 60

Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
80 85 90

Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
110 115 120

Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
140 145 150

Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly

[illegible]

				170					175					180	
Val	Pro	Tyr	Thr	Cys 185	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn	195
Thr	Met	Cys	Gly	Tyr 200	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val	210
Gln	Asp	Val	Ile	Tyr 215	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile	225
Trp	Phe	Met	Asp	Asn 230	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly	240
Ile	Leu	Leu	Pro	Gln 245	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr	255
Ile	Thr	Arg	Val	Glu 260	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp	270
Gly	Leu	Leu	Gly	Pro 275	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly	285
Thr	Gly	Cys	Cys	Leu 290	Cys	Tyr	Pro	Asn							

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<210> 124
<211> 25
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

<400> 124
atcatctatt ccaccgtggt ctggc 25

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<210> 125
<211> 25
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

```
<400> 125
gacagagtgc tccatgatga tgtcc 25
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```
<210> 126
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

<400> 126

<400>	127				
gaggagcggg	ccgaggactc	cagcgtgccc	aggtctggca	tcctgcactt	50
gctgccctct	gacacctggg	aagatggccg	gcccgtggac	cttcacctt	100
ctctgtggtt	tgctggcagc	caccttgatc	caagccaccc	tcagtccac	150
tgcagttctc	atcctcggcc	caaaagtcac	caaagaaaag	ctgacacagg	200
agctgaagga	ccacaacgcc	accagcatcc	tgcagcagct	gccgctgctc	250
agtgccatgc	gggaaaagcc	agccggaggc	atccctgtgc	tgggcagcct	300
ggtgaacacc	gtcctgaagc	acatcatctg	gctgaaggtc	atcacagcta	350
acatcctcca	gctgcaggtg	aagccctcgg	ccaatgacca	ggagctgcta	400
gtcaagatcc	ccctggacat	ggtggctgga	ttcaacacgc	ccctggtcaa	450
gaccatcgtg	gagttccaca	tgacgactga	ggcccaagcc	accatccgca	500
tggacaccag	tgcaagtggc	cccaccgccc	tggctcctcag	tgactgtgcc	550
accagccatg	ggagcctgcg	catccaactg	ctgtataagc	tctccttctt	600
ggtgaacgcc	ttagctaagc	aggtcatgaa	cctcctagtg	ccatccctgc	650
ccaatctagt	gaaaaaccag	ctgtgtcccg	tgatcgaggc	ttccttcaat	700
ggcatgtatg	cagacctcct	gcagctgggtg	aagggtgccca	tttccctcag	750
cattgaccgt	ctggagtttg	accttctgta	tcctgccatc	aagggtgaca	800
ccattcagct	ctacctgggg	gccaaattgt	tggactcaca	gggaaagggtg	850
accaagtggg	tcaataactc	tgcagcttcc	ctgacaatgc	ccaccctgga	900
caacatcccc	ttcagcctca	tcgtgagtca	ggacgtgggtg	aaagctgcag	950
tggctgctgt	gtctcttcca	gaagaattca	tggctcctgtt	ggactctgtg	1000
cttcctgaga	gtgcccatcg	gctgaagtca	agcatcgggc	tgatcaatga	1050
aaaggctgca	gataagctgg	gatctaccca	gatcgtgaag	atcctaactc	1100
aggacactcc	cgagtttttt	atagaccaag	gccatgccaa	ggtggcccaa	1150
ctgatcgtgc	tggaagtgtt	tcctccagt	gaagccctcc	gccctttgtt	1200
caccctgggc	atcgaagcca	gctcggaagc	tcagttttac	accaaagggtg	1250

[illegible]

<210> 128

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
1				5					10					15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
				20					25					30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
				35					40					45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50					55					60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65					70					75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80					85					90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95					100					105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110					115					120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125					130					135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140					145					150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155					160					165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu

170	175	180
Ala Lys Gln Val Met Asn Leu Leu Val	Pro Ser Leu Pro Asn Leu	
185	190	195
Val Lys Asn Gln Leu Cys Pro Val Ile	Glu Ala Ser Phe Asn Gly	
200	205	210
Met Tyr Ala Asp Leu Leu Gln Leu Val	Lys Val Pro Ile Ser Leu	
215	220	225
Ser Ile Asp Arg Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile Lys	
230	235	240
Gly Asp Thr Ile Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp Ser	
245	250	255
Gln Gly Lys Val Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser Leu	
260	265	270
Thr Met Pro Thr Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val Ser	
275	280	285
Gln Asp Val Val Lys Ala Ala Val Ala	Ala Val Leu Ser Pro Glu	
290	295	300
Glu Phe Met Val Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala His	
305	310	315
Arg Leu Lys Ser Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala Asp	
320	325	330
Lys Leu Gly Ser Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp Thr	
335	340	345
Pro Glu Phe Phe Ile Asp Gln Gly His	Ala Lys Val Ala Gln Leu	
350	355	360
Ile Val Leu Glu Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro Leu	
365	370	375
Phe Thr Leu Gly Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr Thr	
380	385	390
Lys Gly Asp Gln Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser Asp	
395	400	405
Arg Ile Gln Leu Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro Asp	
410	415	420
Val Leu Lys Asn Ile Ile Thr Glu Ile	Ile His Ser Ile Leu Leu	
425	430	435
Pro Asn Gln Asn Gly Lys Leu Arg Ser	Gly Val Pro Val Ser Leu	
440	445	450
Val Lys Ala Leu Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr Lys	

455	460	465
Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser		
470	475	480
Pro Val Ser Gln		

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
 gagcgaacat ggcagcgcgt tggcgggtttt ggtgtgtctc tgtgaccatg 50
 gtggtggcgc tgctcatcgt ttgcgacggt ccctcagcct ctgccccaaag 100
 aaagaaggag atggtgttat ctgaaaagggt tagtcagctg atggaatgga 150
 ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
 gtgaaagccc caccgagaaa ttactccggt atcgtcatgt tcaactgctct 250
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
 agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
 ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
 aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaac 450
 ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
 tagacccccca aattatgctg gtccccttat gttgggattg cttttggctg 600
 ttattgggtg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650
 aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
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 atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
 tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850
 aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
 agcgaaagat aatgtgtgtg gctgggtattg gacttgttgt attattcttc 950
 agttggatgc tctctatctt tagatctaaa tatcatggct acccatacag 1000
 ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
 ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100

20										25					30				
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met					
35										40					45				
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys					
50										55					60				
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile					
65										70					75				
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys					
80										85					90				
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg					
95										100					105				
Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp					
110										115					120				
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser					
125										130					135				
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg					
140										145					150				
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln					
155										160					165				
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val					
170										175					180				
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu					
185										190					195				
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met					
200										205					210				
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys					
215										220					225				
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg					
230										235					240				
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn					
245										250					255				
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His					
260										265					270				
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu					
275										280					285				
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys					
290										295					300				
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser					

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<400> 131
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ctgctagggg gagaacgccg gagggaggcg gctggcccgg cggcaggctc 100
tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
cttggcgctg gcggtactgg ccccgaggag aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
atggatggat gtcattggaga ggcatggcta ccgaacacag aaatttgga 500
aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
tggaacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600
taatcttctc cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
ttcaccatct tctggagaaa attttggtat tcaacattt cacacatctc 800
tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850
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tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100

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gcatgtacga	ggctagtgc	catgttcgc	ttttgatgat	gggaccagga	1150
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ccctaccatg	cttgatattg	ctggaattcc	tctgcctcag	aacctgagtg	1250
gatactcttt	gttgccgtta	tcatcagaaa	catttaagaa	tgaacataaa	1300
gtcaaaaacc	tgcattccacc	ctggattctg	agtgaattcc	atggatgtaa	1350
tgtgaatgcc	tccacctaca	tgcttcgaac	taaccactgg	aaatatatag	1400
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ttctttggat	cagaagcttc	attccattat	aaactaccct	aaagtttctg	1550
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atgaaacagt	tttaataatt	accaagtttt	ggccgggcac	agtggctcac	1850
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aagagattga	gaccatcctg	gccaacatgg	tgaaaccctg	tctctactaa	1950
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tgtgtcgcaa	aaaaataaaa	ataaaataat	aataattacc	aatttttcat	2150
tattttgtaa	gaatgtagtg	tatttttaaga	taaaatgcca	atgattataa	2200
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aacaatttag	tggaagtatc	aaaaggattg	aagcaaatac	tgtaacagtt	2300
atgttccttt	aaataataga	gaatataaaa	tattgtaata	atatgtatca	2350
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<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

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Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45

Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60

Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly
80 85 90

Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu
95 100 105

Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly
110 115 120

Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His
125 130 135

His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala
140 145 150

Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg
155 160 165

Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr
170 175 180

Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr
185 190 195

Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr
200 205 210

Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His
215 220 225

Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
230 235 240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr
245 250 255

Tyr	Ser	Ser	Tyr	Thr 260	Lys	Asn	Cys	Thr	Gly 265	Arg	Phe	Thr	Lys	Lys 270
Glu	Ile	Lys	Asn	Ile 275	Arg	Ala	Phe	Tyr	Tyr 280	Ala	Met	Cys	Ala	Glu 285
Thr	Asp	Ala	Met	Leu 290	Gly	Glu	Ile	Ile	Leu 295	Ala	Leu	His	Gln	Leu 300
Asp	Leu	Leu	Gln	Lys 305	Thr	Ile	Val	Ile	Tyr 310	Ser	Ser	Asp	His	Gly 315
Glu	Leu	Ala	Met	Glu 320	His	Arg	Gln	Phe	Tyr 325	Lys	Met	Ser	Met	Tyr 330
Glu	Ala	Ser	Ala	His 335	Val	Pro	Leu	Leu	Met 340	Met	Gly	Pro	Gly	Ile 345
Lys	Ala	Gly	Leu	Gln 350	Val	Ser	Asn	Val	Val 355	Ser	Leu	Val	Asp	Ile 360
Tyr	Pro	Thr	Met	Leu 365	Asp	Ile	Ala	Gly	Ile 370	Pro	Leu	Pro	Gln	Asn 375
Leu	Ser	Gly	Tyr	Ser 380	Leu	Leu	Pro	Leu	Ser 385	Ser	Glu	Thr	Phe	Lys 390
Asn	Glu	His	Lys	Val 395	Lys	Asn	Leu	His	Pro 400	Pro	Trp	Ile	Leu	Ser 405
Glu	Phe	His	Gly	Cys 410	Asn	Val	Asn	Ala	Ser 415	Thr	Tyr	Met	Leu	Arg 420
Thr	Asn	His	Trp	Lys 425	Tyr	Ile	Ala	Tyr	Ser 430	Asp	Gly	Ala	Ser	Ile 435
Leu	Pro	Gln	Leu	Phe 440	Asp	Leu	Ser	Ser	Asp 445	Pro	Asp	Glu	Leu	Thr 450
Asn	Val	Ala	Val	Lys 455	Phe	Pro	Glu	Ile	Thr 460	Tyr	Ser	Leu	Asp	Gln 465
Lys	Leu	His	Ser	Ile 470	Ile	Asn	Tyr	Pro	Lys 475	Val	Ser	Ala	Ser	Val 480
His	Gln	Tyr	Asn	Lys 485	Glu	Gln	Phe	Ile	Lys 490	Trp	Lys	Gln	Ser	Ile 495
Gly	Gln	Asn	Tyr	Ser 500	Asn	Val	Ile	Ala	Asn 505	Leu	Arg	Trp	His	Gln 510
Asp	Trp	Gln	Lys	Glu 515	Pro	Arg	Lys	Tyr	Glu 520	Asn	Ala	Ile	Asp	Gln 525
Trp	Leu	Lys	Thr	His 530	Met	Asn	Pro	Arg	Ala 535	Val				

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<400> 133
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ctacatccta ggcctttctg ggcttttggg cacactgggt gccatgctgc 200
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
gttggtttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
catcaccagc tgtgacatct atagcaccct tctgggcctg cccgtgaca 350
tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctctccctg 400
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450
atccccagcc aaagacagag tggcggtagc aggtggagtc ttttcatcc 500
ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggac 550
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cagggtatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct 850
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agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

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cctccaaaga aactgattgg ccctggaacc tccatcccac tcttggtatg 1350
 actccacagt gtccagacta atttgatcat gaactgaaat aaaaccatcc 1400
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 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
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 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly
 50 55 60
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
 65 70 75
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
 80 85 90
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
 95 100 105
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala
 110 115 120
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
 125 130 135
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
 140 145 150
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
 155 160 165
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
 170 175 180
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
 185 190 195
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
 200 205 210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
215 220 225

Leu Thr Gly Tyr Val
230

<210> 135
<211> 610
<212> DNA
<213> Homo sapiens

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aagtcacgc tcccgtggc tcagaacct ggctgtgcca gccggcacc 150
aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
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atctcccatc tccagtaaag gtgaaagcag aagacgtttt cctgagaag 400
acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
acctgtaaaa 610

<210> 136
<211> 119
<212> PRT
<213> Homo sapiens

<400> 136
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
20 25 30
Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
35 40 45
Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
50 55 60
Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

	65		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
			95						100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
			110						115					

<210> 137
<211> 771
<212> DNA
<213> Homo sapiens

<400> 137
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agtggcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
gtggggacaa gttctacgac cccctgcagc actggtgcta tgatgatgcc 200
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agaactgca ctcagcccg accctcgatg acaggctttg tcgcagtgtc 350
agctaattga acatcagggg aacgatgact cctggattct ccttcctggg 400
tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
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atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
tatgtacttt ataatgaaa a 771

<210> 138
<211> 110
<212> PRT
<213> Homo sapiens

<400> 138
Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
1 5 10 15

<400> 140

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Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu Asp	
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu	Val Ile	
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ccttctgccc ctctttctct gccaccgct gcttctggc 150
 ccttctccga ccccgctcta gcagcagacc tcttgggggc tgtgggttga 200
 tctgtggccc ctgtgctctc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccg accagcggcc tgacctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tctccttgc tgggactcgc gctgctctgg ttccccctgg 350
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 agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450
 gatgtactgc ctgcgtgta cctgctcaga gggcgcccat gtgagttgtt 500
 accgcctcca ctgtccgct gtccactgcc cccagcctgt gacggagcca 550
 cagcaatgct gtcccaagtg tgtggaacct cacactcct ctggactccg 600
 ggccccacca aagtccctgcc agcacaacgg gacctgtac caacacggag 650
 agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700
 gtctctgca gctgcacaga gggccagatc tactgaggcc tcacaacctg 750
 cccgaacca ggctgcccag caccctccc actgccagac tctgctgcc 800
 aagcctgcaa agatgaggca agtgagcaat cgatgaaga ggacagtgtg 850
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
 tgggagaaa agaggcccg gcacccagc cccactggc ctcagcgccc 950
 ctctgagctt catcctcgc cacttcagac ccaagggagc aggcagcaca 1000
 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
 cgggaagacg tactccacg gggaggtgtg gcacccggcc ttccgtgct 1100

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<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
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<400> 142
Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
 1          5          10          15

Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
          20          25          30

Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
          35          40          45

Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
          50          55          60

Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
          65          70          75

Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
          80          85          90

Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
          95          100          105

Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
          110          115          120

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Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro
				125					130					135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys
				140					145					150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro
				155					160					165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu
				170					175					180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg
				185					190					195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly
				200					205					210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe
				215					220					225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val
				230					235					240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly
				245					250					255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg
				260					265					270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly
				275					280					285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys
				290					295					300
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro
				305					310					315
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg
				320					325					330
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser
				335					340					345
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala
				350					355					360
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu
				365					370					375
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His
				380					385					390
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala
				395					400					405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
440 445 450

Thr

<210> 143
<211> 693
<212> DNA
<213> Homo sapiens

<400> 143
ctagcctgcg ccaaggggta gtgagaccgc gcggaacag cttgcggctg 50
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cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
tgggctacgc gtcctcgtt atcgtgaccc cggaagagcg gcggaagcag 200
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
ggcgccagcg ggaggtcacc gtgagaccgg acttgctcc gtgggcgccc 400
gaccttggt tgggcgcagg aatccgaggc agcctttctc ctctgtgggc 450
ccagcggaga gtccggaccg agataccatg ccaggactct ccggggctct 500
gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
tttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
<211> 93
<212> PRT
<213> Homo sapiens

<400> 144
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
1 5 10 15
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90
Arg Ser Pro														

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 ttgaggggaa gaggtgact gtacgttctt tctactctgg caccactctc 100
 caggctgcca tggggcccag caccctcttc ctcatcttgt tctttttgtc 150
 atggtcgagg cccctccaag gacagcagca ccaccttgtg gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcaactcaga actgaggccg 350
 acaccatctc cgggagagt gacgtctctg agcgggaggt agactatctg 400
 gagaccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
 tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
 tggtagacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
 gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650
 ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700
 gcttcccag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
 aaccgaacag tggtggacag ctcaagtatt ccagcagagg ggctgatccc 900

	335		340		345
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala					
	350		355		360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu					
	365		370		375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly					
	380		385		390
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu					
	395		400		405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttctctgtc tcttaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500
 ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650
 tgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca ggttacagat 850

aggagataacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaataact ctgctgtggc ctatTTTTtg gcattgttgg actgaagatt 950
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcaccoga agctctgctt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tggtggcttc tcagagtttc caagcaggga 1200
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 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaatcc ccgttttacc agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
 aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaaggagg cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tctcacagg 1650
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700
 acattcttct ttagggatat taaggctctt ctcccagatc caaagtcccg 1750
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850
 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950
 tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
 acagagtgtg tcctaattgt ttgttcatta tattacactt tcagtaaaaa 2050
 aa 2052

<210> 148
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1	5	10	15
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala	20	25	30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys	35	40	45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe	50	55	60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe	65	70	75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp	80	85	90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr	95	100	105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser	110	115	120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly	125	130	135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile	140	145	150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg	170	175	180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu	185	190	195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His	200	205	210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp	215	220	225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu	230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys	245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys			

tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250

agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys	1	5	10	15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro	170	175	180	
Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn	185	190	195	
Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr	200	205	210	
Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys	215	220	225	
Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu	230	235	240	

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255

Cys Asn Arg

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
aactgctctg tggttggaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cagtcacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 156
aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
ttctggcttt ggtctcggtg ccagggccc aggccgtgtg gttgggaaga 100
ctggacctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
ccgggaaaag ggctttgcc aaggagaagga catgaagaac gtcgtggggg 200
tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
tgctggccac caacttcaga gactatgcca tcattctcac tcagctggag 400
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
gcttctgtgc acagtagcag gccagctgc agaaggacct cacctgtgct 550
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
gggtcctgtg acctcgcca gtgtccacc acctcgctca gcggctcccg 650
gggccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
<211> 163
<212> PRT
<213> Homo sapiens

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
1 5 10 15
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
20 25 30
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
35 40 45
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
50 55 60
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
65 70 75
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90
Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105
Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120
Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135
Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150
Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159

<211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
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 gtaaaactgct gacgatgcag agttccgtga cgggtgcagga aggctgtgt 150
 gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttaccc 200
 tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
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 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
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 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600
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 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgc 850
 tggctgtgac agttgatgca gttgacagca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950
 ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100
 tggagccaca gccctggtct tctgtcctt ctgcgtcatc ttcgtttag 1150
 tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctacggggcc 1250
 cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg Ser
	185	190 195
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr Ser
	200	205 210
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr Asn
	215	220 225
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu Thr
	230	235 240
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu Gly
	245	250 255
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg Leu
	260	265 270
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg Leu
	275	280 285
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro Ser
	290	295 300
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp Ala
	305	310 315
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln Gln
	320	325 330
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly Val
	335	340 345
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val Phe
	350	355 360
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg Lys
	365	370 375
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile Glu
	380	385 390
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu Thr
	395	400 405
Glu Pro Trp Ala	Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro Ala
	410	415 420
Ser Ala Arg Ser	Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala Ser
	425	430 435
Leu Ser Phe Gln	Met Val Lys Pro Trp	Asp Ser Arg Gly Gln Glu
	440	445 450
Ala Thr Asp Thr	Glu Tyr Ser Glu Ile	Lys Ile His Arg
	455	460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
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 accctgttcc tgggtgtcac gctcggcctg gccgctgcc tgctcttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gaggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat totgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagc caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650
 gctcccacc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
 20 25 30
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
 35 40 45
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
 50 55 60
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
 65 70 75

Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr
80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro
95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly
110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr
125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser
155 160 165

Cys Val Pro Glu His
170

<210> 163
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 163
ggagatgaag accctgttcc tg 22

<210> 164
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 164
ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga cttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtccttca ccctggagga ggaggatatt acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcacgagg 50
cagaggtctc acagcagcca aggaacctgg ggcccgtctc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgtcat cgtccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccgacag cactgagtc cttccccac cccggttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500

Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 171
 ggctgcggga ctggaagtca tcggg 25

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 172
 ctccaggcca tgaggattct gcag 24

<210> 173
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
cgtgtagaca ccaggctttc gggcg 25

<210> 176
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
cccttgatga tcctgggc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aacctgcat ttcttattca 50
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150
agaaaactgc tctaagacaa gcaagaagg agacctacta aatgccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400
ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
tgtgaccaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcataatc aggatgcagt 600
tttagaagat atttttaaga agaatgacca tgatgggtgat ggcttcattt 650
ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
atttctactt ttttttttta gctatttact gtactttatg tataaaaca 750
agtcactttt ctccaagttg tatttgctat ttttcccta tgagaagata 800
tttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850
ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				215	220	

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgtttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 183
cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcatcctgat atgacttggt acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 187

gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaaccaa acttctctgtg ctaagtgcc 100

cccaaatgct tctgtgtca ataactca ctgcacctgc aaccatggat 150

atacttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttcttgtttc atttcgcgac tgccctctca gtgtttctctg ggatccccctc 550

ccaaataaag tacttatatt etc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
1 5 10 15

Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 190
 agggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 191
 cgttacatgt ctccaagggg aatg 24

<210> 192
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 192
 cctgtgctaa gtgccccca aatgcttctt gtgtcaataa cactcactgc 50

<210> 193
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<400> 193
 caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
 ggtggggggc acagggaaaag ggtgacctct gagattcccc ttttccccca 100
 gactttggaa gtgaccacc atggggctca gcatcttttt gtcctgtgt 150
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
 gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
 gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
 gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
 cccatcccg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgccgcgta accagcagcg ttcaaccct 500
 gccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
 gctggggcat caccaaccac ccacggaacc cattcccgga tctgctccag 600
 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
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 atgcctgcca ggggtattct gggggccccc tgggtgtgtgg gggagtcctt 750
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800
 ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatacttc 950
 ccctagctcc actcttgttg gcttggaac ttcttggaac tttaactcct 1000
 gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120

Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
125 130 135

Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
140 145 150

Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
155 160 165

Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
170 175 180

Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
185 190 195

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu
200 205 210

Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp
215 220 225

Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp
230 235 240

Ile Arg Met Ile Met Arg Asn Asn
245

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
gcggccacac gcagctagcc ggagcccga ccaggcgccct gtgcctcctc 50
ctcgtccctc gccgcgtccg cgaagcctgg agccggcgagg agccccgcgc 100
tcgcatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgctc 150
ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
tcagtgcac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
cggtcggctg tctcaagtt agtcatgatg ttggaaggaa aagccaacga 500
gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
tgccctgagg accccgctg gactccccag ccttcccacc ccatacctcc 600

ctcccgatct tgetgccctt cttgacacac tgtgatctct ctctctctca 650
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 agcacaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750
 ttgggtcccc tccctctctt ctccctctct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850
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 tcagaaagtc tccaagccaa gttagagctc actgacctgg ctctgacgag 950
 gacccaggc cactctgaga agaccttga gttagggaca ggctgcaggg 1000
 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050
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 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tgggggtttg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgct 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75

caatgccaac	tccatctcct	gcccttcgcc	ctgcacgtgc	agcaataaca	950
tcgtggactg	tcgaggaaag	ggcttgatgg	agattcctgc	caacttgccg	1000
gagggcatcg	tcgaaatacg	cctagaacag	aactccatca	aagccatccc	1050
tgcaggagcc	ttcacccagt	acaagaaact	gaagcgaata	gacatcagca	1100
agaatcagat	atcggatatt	gtccagatg	ccttcagggg	cctgaaatca	1150
ctcacatcgc	tggctcctgta	tgggaacaag	atcaccgaga	ttgccaaggg	1200
actgtttgat	gggctgggtg	ccctacagct	gtctctctc	aatgccaaaca	1250
agatcaactg	cctgcgggtg	aacacgtttc	aggacctgca	gaacctcaac	1300
ttgctctccc	tgtatgacaa	caagctgcag	accatcagca	aggggctctt	1350
cgcccctctg	cagtccatcc	agacactcca	cttagcccaa	aacccatttg	1400
tgtgcgactg	ccacttgaag	tggctggccg	actacctcca	ggacaacccc	1450
atcgagacaa	gcggggcccg	ctgcagcagc	ccgcgccgac	tcgccaacaa	1500
gcgcacacgc	cagatcaaga	gcaagaagtt	ccgctgctca	ggctccgagg	1550
attaccgcag	caggttcagc	agcgagtgt	tcatggacct	cgtgtgcccc	1600
gagaagtgtc	gctgtgaggg	cacgattgtg	gactgctcca	accagaagct	1650
ggctccgcac	ccaagccacc	tcctgaata	tgtcaccgac	ctgcgactga	1700
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cccaacctgc	ggaaaataaa	tctgagtaac	aataagatca	aggaggtgcg	1800
agagggagct	ttcgatggag	cagccagcgt	gcaggagctg	atgctgacag	1850
ggaaccagct	ggagaccgtg	cacgggcgcg	tgttcctggg	cctcagtggc	1900
ctcaaaacct	tgatgctgag	gagtaacttg	atcagctgtg	tgagtaatga	1950
cacctttgcc	ggcctgagtt	cggtgagact	gctgtccctc	tatgacaatc	2000
ggatcaccac	catcacccct	ggggccttca	ccacgcttgt	ctccctgtcc	2050
accataaacc	tcctgtccaa	ccccttcaac	tgcaactgcc	acctggcctg	2100
gctcggcaag	tggttgagga	agaggcggat	cgtcagtggg	aaccctaggt	2150
gccagaagcc	atTTTTctc	aaggagattc	ccatccagga	tgtggccatc	2200
caggacttca	cctgtgatgg	caacgaggag	agtagctgcc	agctgagccc	2250
gcgctgcccc	gagcagtgca	cctgtatgga	gacagtgggtg	cgatgcagca	2300
acaaggggct	ccgcgccctc	cccagaggca	tgcccaagga	tgtgaccgag	2350

ctgtacctgg aaggaaacca cctaacagcc gtgcccagag agctgtccgc 2400
cctccgacac ctgacgctta ttgacctgag caacaacagc atcagcatgc 2450
tgaccaatta caccttcagt aacatgtctc acctctccac tctgatcctg 2500
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Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg			
				65					70					75			
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu			
				80					85					90			
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe			
				95					100					105			
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys			
				110					115					120			
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu			
				125					130					135			
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg			
				140					145					150			
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp			
				155					160					165			
Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu			
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Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu			
				200					205					210			
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp			
				215					220					225			
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr			
				230					235					240			
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp			
				245					250					255			
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro			
				260					265					270			
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr			
				275					280					285			
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu			
				290					295					300			
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu			
				305					310					315			
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr			

605					610					615				
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
				650					655					660
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750
Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr
				755					760					765
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile
				770					775					780
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe
				785					790					795
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg
				800					805					810
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu
				815					820					825
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu
				830					835					840
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly
				845					850					855
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu
				860					865					870
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser
				875					880					885
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr

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<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
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 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
gcaggctttg aggatgaagg ctgc 24

<210> 205
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 207
tcagtgacca aggctgagca ggcg 24

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 208

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<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatctt actgtcactt ccagatctg cttctcacca 250
agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
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catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaattgtga 650
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Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg	170		175		180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val	185		190		195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe	200		205		210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val	215		220		225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu	230		235		240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly	245		250		255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu	260		265		270
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg	275		280		285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg	290		295		300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr	305		310		315
Arg Tyr Val Thr Lys Leu Leu Val	320				

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 <211> 1554
 <212> DNA
 <213> Homo sapiens

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 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200
 tttgcatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctcgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala	20	25	30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu	35	40	45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn	50	55	60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg	65	70	75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His	80	85	90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys	95	100	105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn	110	115	120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu	125	130	135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu	140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser	155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val	170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln	185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu	200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu	215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys	230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser	245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser	260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys	275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys	290	295	300

Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val
305 310 315

Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu
320 325 330

Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln
335 340 345

Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg
350 355 360

Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro
365 370 375

Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp
380 385 390

Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly
395 400 405

Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr
410 415 420

Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val
425 430 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

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cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt ccccccgag gaggatgaca agcaggacat tcagctggtg 250
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aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
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20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
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<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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 aataaagctt gcccggggc a 1871

<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218
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 Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
 20 25 30
 Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35 40 45

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<212> PRT
<213> Homo sapiens

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35 40 45
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
50 55 60
Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
65 70 75
Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
80 85 90
Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
95 100 105
Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
110 115 120
Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
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Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
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Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
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Pro	Cys	Ser	Val	Ile 200	Ser	Ile	Gln	Asp	Val 205	Leu	Cys	Pro	Val	Tyr 210
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Cys	Gly	Gly	Ser	Leu 260	Pro	Phe	Tyr	Pro	Phe 265	Ala	Glu	Asp	Glu	Pro 270
Val	Asp	Gln	Gly	His 275	Arg	Gln	Lys	Thr	Leu 280	Ser	Val	Leu	Val	Ser 285
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Leu	Gly	Ile	Phe	Leu 305	Ser	Phe	Tyr	Leu	Leu 310	Thr	Val	Leu	Leu	Ala 315
Cys	Trp	Glu	Asn	Trp 320	Arg	Gln	Lys	Lys	Lys 325	Thr	Leu	Leu	Val	Ala 330
Ile	Asp	Arg	Ala	Cys 335	Pro	Glu	Ser	Gly	His 340	Pro	Arg	Val	Leu	Ala 345
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Ser	Phe	Glu	Asn	Val 365	Ser	Gly	Ser	Thr	Asp 370	Gly	Leu	Val	Asp	Ser 375
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Glu	Pro	Val	Gly	Thr 395	Arg	Pro	Arg	Val	Asp 400	Ser	Met	Ser	Ser	Val 405
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PC26073

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<212> DNA
<213> Homo sapiens
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<212> PRT
<213> Homo sapiens

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35 40 45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp
50 55 60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser
65 70 75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala

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Asp	Gln	Val	Pro	His 125	Phe	Ser	Gln	Ala	Ile 130	Tyr	Arg	Ala	Arg	Leu 135
Ser	Arg	Gly	Thr	Arg 140	Pro	Gly	Ile	Pro	Phe 145	Leu	Phe	Leu	Glu	Ala 150
Ser	Asp	Arg	Asp	Glu 155	Pro	Gly	Thr	Ala	Asn 160	Ser	Asp	Leu	Arg	Phe 165
His	Ile	Leu	Ser	Gln 170	Ala	Pro	Ala	Gln	Pro 175	Ser	Pro	Asp	Met	Phe 180
Gln	Leu	Glu	Pro	Arg 185	Leu	Gly	Ala	Leu	Ala 190	Leu	Ser	Pro	Lys	Gly 195
Ser	Thr	Ser	Leu	Asp 200	His	Ala	Leu	Glu	Arg 205	Thr	Tyr	Gln	Leu	Leu 210
Val	Gln	Val	Lys	Asp 215	Met	Gly	Asp	Gln	Ala 220	Ser	Gly	His	Gln	Ala 225
Thr	Ala	Thr	Val	Glu 230	Val	Ser	Ile	Ile	Glu 235	Ser	Thr	Trp	Val	Ser 240
Leu	Glu	Pro	Ile	His 245	Leu	Ala	Glu	Asn	Leu 250	Lys	Val	Leu	Tyr	Pro 255
His	His	Met	Ala	Gln 260	Val	His	Trp	Ser	Gly 265	Gly	Asp	Val	His	Tyr 270
His	Leu	Glu	Ser	His 275	Pro	Pro	Gly	Pro	Phe 280	Glu	Val	Asn	Ala	Glu 285
Gly	Asn	Leu	Tyr	Val 290	Thr	Arg	Glu	Leu	Asp 295	Arg	Glu	Ala	Gln	Ala 300
Glu	Tyr	Leu	Leu	Gln 305	Val	Arg	Ala	Gln	Asn 310	Ser	His	Gly	Glu	Asp 315
Tyr	Ala	Ala	Pro	Leu 320	Glu	Leu	His	Val	Leu 325	Val	Met	Asp	Glu	Asn 330
Asp	Asn	Val	Pro	Ile 335	Cys	Pro	Pro	Arg	Asp 340	Pro	Thr	Val	Ser	Ile 345
Pro	Glu	Leu	Ser	Pro 350	Pro	Gly	Thr	Glu	Val 355	Thr	Arg	Leu	Ser	Ala 360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr

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Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala					
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Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu					
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Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met					
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Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val					
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Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile					
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Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro					
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Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu					
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Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr					
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Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val					
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Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser					
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His	Glu	Val	Val	Val	Val	Gln	Ser	Val	Val	Ala	Lys	Leu	Val	Gly					
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Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val					
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Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu					
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Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr					
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Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu					
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Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly					
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Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp					
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Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu					
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Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val				
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Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr				
	695	700		705	
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile				
	710	715		720	
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val				
	725	730		735	
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg				
	740	745		750	
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val				
	755	760		765	
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile				
	770	775		780	
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 231
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<210> 232
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 <212> DNA

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 $\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

4007-255

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<211> 421

<212> PRT

<213> Homo sapiens

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Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
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Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
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Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165
Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile
				170					175					180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala
				185					190					195

Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr	Ser
200		205	210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn	Pro
215		220	225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg	Lys
230		235	240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp	Pro
245		250	255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser	Asp
260		265	270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser	Glu
275		280	285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly	Asn
290		295	300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu	Met
305		310	315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu	Glu
320		325	330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser	Val
335		340	345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val	Tyr
350		355	360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly	Ile
365		370	375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr	Gly
380		385	390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu	Thr
395		400	405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn	Leu
410		415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235
 caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50
 tgttccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100

[illegible]

Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe
	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met
	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn
	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe
	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala
	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys
	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser
	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala
	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser
	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser
	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile
	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn
	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile
	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	
	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttgccctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

ggctgaccgt gctacattgc ctggaggaag cctaagggaac ccaggcatcc 50

agctgccac gctgagtc aagattcttc ccaggaacac aaacgtagga 100

gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaaatg	ttctccttat	gtttgggtcta	ctattgcatt	tagaagctgc	300
aacaaattcc	aatgagacta	gcacctctgc	caacactgga	tccagtgtga	350
tctccagtgg	agccagcaca	gccaccaact	ctgggtccag	tgtgacctcc	400
agtgggggtca	gcacagccac	catctcaggg	tccagcgtga	cctccaatgg	450
ggtcagcata	gtcaccaact	ctgagttcca	tacaacctcc	agtgggatca	500
gcacagccac	caactctgag	ttcagcacag	cgtccagtgg	gatcagcata	550
gccaccaact	ctgagtccag	cacaacctcc	agtggggcca	gcacagccac	600
caactctgag	tccagcacac	cctccagtgg	ggccagcaca	gtcaccaact	650
ctgggtccag	tgtgacctcc	agtggagcca	gcaactgccac	caactctgag	700
tccagcacag	tgtccagttag	ggccagcact	gccaccaact	ctgagtctag	750
cacactctcc	agtggggcca	gcacagccac	caactctgac	tccagcacaa	800
cctccagtgg	ggctagcaca	gccaccaact	ctgagtccag	cacaacctcc	850
agtggggcca	gcacagccac	caactctgag	tccagcacag	tgtccagttag	900
ggccagcact	gccaccaact	ctgagtccag	cacaacctcc	agtggggcca	950
gcacagccac	caactctgag	tccagaacga	cctccaatgg	ggctggcaca	1000
gccaccaact	ctgagtccag	cacgacctcc	agtggggcca	gcacagccac	1050
caactctgac	tccagcacag	tgtccagtgg	ggccagcact	gccaccaact	1100
ctgagtccag	cacgacctcc	agtggggcca	gcacagccac	caactctgag	1150
tccagcacga	cctccagtgg	ggctagcaca	gccaccaact	ctgactccag	1200
cacaacctcc	agtggggccg	gcacagccac	caactctgag	tccagcacag	1250
tgtccagtgg	gatcagcaca	gtcaccaatt	ctgagtccag	cacacctcc	1300
agtggggcca	acacagccac	caactctgag	tccagtacga	cctccagtgg	1350
ggccaacaca	gccaccaact	ctgagtccag	cacagtgtcc	agtggggcca	1400
gcaactgccac	caactctgag	tccagcacaa	cctccagtgg	ggtcagcaca	1450
gccaccaact	ctgagtccag	cacaacctcc	agtggggcta	gcacagccac	1500
caactctgac	tccagcacaa	cctccagtga	ggccagcaca	gccaccaact	1550
ctgagtctag	cacagtgtcc	agtgggatca	gcacagtcac	caattctgag	1600
tccagcacaa	cctccagtgg	ggccaacaca	gccaccaact	ctgggtccag	1650
tgtgacctct	gcaggctctg	gaacagcagc	tctgactgga	atgcacacaa	1700

<400> 243															
Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu	
1				5					10					15	
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser	
				20					25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				35					40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala	
				50					55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val	
				65					70					75	
Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	110	115	120
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val	125	130	135
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala	140	145	150
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	155	160	165
Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala	170	175	180
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	185	190	195
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	200	205	210
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	215	220	225
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	230	235	240
Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala	245	250	255
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	260	265	270
Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	275	280	285
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	290	295	300
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	305	310	315
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala	320	325	330
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	335	340	345
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala	350	355	360
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380	385	390

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala
395 400 405

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
410 415 420

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala
425 430 435

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
440 445 450

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
455 460 465

Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala
470 475 480

Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala
485 490 495

Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile
500 505 510

Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe
515 520 525

Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn
530 535 540

Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly
545 550 555

Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro
560 565 570

Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile
575 580 585

Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro
590 595

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50
 ttcccgacct tcccagcaat atgcatcttg cagctctggt cggctcctgc 100
 tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150
 cccattgag aagggtcattg aagggatcaa ccgagggctg agcaatgcag 200
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
 gccggaaggg aagtggagaa gggtttcaac ggacttagca acatggggag 300
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350
 tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400
 gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450
 gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500
 ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550
 caggctggaa aggaagtga gaagcttggc caaggtgccc accatgctgc 600
 tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcgatct 700
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
 agtcaacacg cttttcatca accttccgc cctgtggagg agcgtcgcca 800

215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg		
230	235	240
Ser Val Ala Asn Ile Met Pro		
245		

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 249
 caatatgcat cttgcacgtc tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 251
 tgacccatt gagaaggta ttgaaggat caaccgagg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

<400> 252
 ctccgggtcc ccaggggctg cgcggggccg gcctggcaag ggggacgagt 50
 cagtggacac tccaggaaga gcggccccgc ggggggagat gaccgtgcgc 100
 tgaccctgac tcaactcagg tccggaggcg ggggcccccg gggcgactcg 150
 ggggaggacc gcggggcgga gctgccgcc gtgagtcagg ccgagccacc 200
 tgagcccgag ccgcgggaca ccgtcgtcc tgctctccga atgctgcgca 250

(The following information was obtained from the records of the Federal Bureau of Investigation, Department of Justice.)

ggagctgcag atcttctcat cgggacagcc cgtgcagaat ctgctcctgg 1750
 acacccacag ggggctgctg tatgcgccct cacactcggg cgtagtccag 1800
 gtgcccattgg ccaactgcag cctgtaccgg agctgtgggg actgcctcct 1850
 cgccccgggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900
 gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950
 ggagccagcg ccaaggacct ttgcagcgcg tcttcgggtt tgteccccgtc 2000
 ttttgtacca acaggggaga agccatgtga gcaagtccag ttccagccca 2050
 acacagtga cactttggcc tgcccgtcc tctccaacct ggcgaccga 2100
 ctctggctac gcaacggggc ccccgtaat gcctcggcct cctgccacgt 2150
 gctaccact ggggacctgc tgctggtggg caccacaacag ctgggggagt 2200
 tccagtgtg gtcactagag gagggcttcc agcagctgg agccagctac 2250
 tgcccagagg tgggtggagga cggggtggca gaccaaacag atgaggggtg 2300
 cagtgtaccc gtcattatca gcacatcgcg tgtgagtga ccagctggtg 2350
 gcaaggccag ctggggtgca gacaggtcct actggaagga gttcctggtg 2400
 atgtgcacgc tctttgtgct ggccgtgctg ctcccagttt tattcttgct 2450
 ctaccggcac cggaacagca tgaaagtctt cctgaagcag ggggaatgtg 2500
 ccagcgtgca ccccaagacc tgccctgtgg tgctgcccc tgagaccgc 2550
 ccactcaacg gcctagggcc ccctagcacc ccgtcgcac accgagggta 2600
 ccagtccctg tcagacagcc ccccgggggc ccgagtcttc actgagtcag 2650
 agaagaggcc actcagcacc caagacagct tcgtggaggt atccccagt 2700
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 acgaccgtgg tgccccggcc ttgggagcct tggagccagc tggcctgctg 2900
 ctctccagtc aagtagcgaa gtcctacca ccagacacc caaacagccg 2950
 tggccccaga ggtcctggcc aaatatgggg gcctgcctag gttggtggaa 3000
 cagtgtcct tatgtaaact gagcccttg tttaaaaaac aattccaaat 3050
 gtgaaactag aatgagaggg aagagatagc atggcatgca gcacacacgg 3100

Ser	Phe	Lys	Gly	Lys 125	Asp	Pro	Gln	Arg	Asp 130	Cys	Gln	Asn	Tyr	Ile 135
Lys	Ile	Leu	Leu	Pro 140	Leu	Ser	Gly	Ser	His 145	Leu	Phe	Thr	Cys	Gly 150
Thr	Ala	Ala	Phe	Ser 155	Pro	Met	Cys	Thr	Tyr 160	Ile	Asn	Met	Glu	Asn 165
Phe	Thr	Leu	Ala	Arg 170	Asp	Glu	Lys	Gly	Asn 175	Val	Leu	Leu	Glu	Asp 180
Gly	Lys	Gly	Arg	Cys 185	Pro	Phe	Asp	Pro	Asn 190	Phe	Lys	Ser	Thr	Ala 195
Leu	Val	Val	Asp	Gly 200	Glu	Leu	Tyr	Thr	Gly 205	Thr	Val	Ser	Ser	Phe 210
Gln	Gly	Asn	Asp	Pro 215	Ala	Ile	Ser	Arg	Ser 220	Gln	Ser	Leu	Arg	Pro 225
Thr	Lys	Thr	Glu	Ser 230	Ser	Leu	Asn	Trp	Leu 235	Gln	Asp	Pro	Ala	Phe 240
Val	Ala	Ser	Ala	Tyr 245	Ile	Pro	Glu	Ser	Leu 250	Gly	Ser	Leu	Gln	Gly 255
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Ser 265	Glu	Thr	Gly	Gln	Glu 270
Phe	Glu	Phe	Phe	Glu 275	Asn	Thr	Ile	Val	Ser 280	Arg	Ile	Ala	Arg	Ile 285
Cys	Lys	Gly	Asp	Glu 290	Gly	Gly	Glu	Arg	Val 295	Leu	Gln	Gln	Arg	Trp 300
Thr	Ser	Phe	Leu	Lys 305	Ala	Gln	Leu	Leu	Cys 310	Ser	Arg	Pro	Asp	Asp 315
Gly	Phe	Pro	Phe	Asn 320	Val	Leu	Gln	Asp	Val 325	Phe	Thr	Leu	Ser	Pro 330
Ser	Pro	Gln	Asp	Trp 335	Arg	Asp	Thr	Leu	Phe 340	Tyr	Gly	Val	Phe	Thr 345
Ser	Gln	Trp	His	Arg 350	Gly	Thr	Thr	Glu	Gly 355	Ser	Ala	Val	Cys	Val 360
Phe	Thr	Met	Lys	Asp 365	Val	Gln	Arg	Val	Phe 370	Ser	Gly	Leu	Tyr	Lys 375
Glu	Val	Asn	Arg	Glu 380	Thr	Gln	Gln	Trp	Tyr 385	Thr	Val	Thr	His	Pro 390
Val	Pro	Thr	Pro	Arg 395	Pro	Gly	Ala	Cys	Ile 400	Thr	Asn	Ser	Ala	Arg 405

Glu Arg Lys Ile Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val Leu
410	415 420
Asn Phe Leu Lys Asp His Phe Leu Met	Asp Gly Gln Val Arg Ser
425	430 435
Arg Met Leu Leu Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val Ala
440	445 450
Val His Arg Val Pro Gly Leu His His	Thr Tyr Asp Val Leu Phe
455	460 465
Leu Gly Thr Gly Asp Gly Arg Leu His	Lys Ala Val Ser Val Gly
470	475 480
Pro Arg Val His Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser Gly
485	490 495
Gln Pro Val Gln Asn Leu Leu Leu Asp	Thr His Arg Gly Leu Leu
500	505 510
Tyr Ala Ala Ser His Ser Gly Val Val	Gln Val Pro Met Ala Asn
515	520 525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg Asp
530	535 540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser	Cys Lys His Val Ser Leu
545	550 555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile Glu
560	565 570
Gly Ala Ser Ala Lys Asp Leu Cys Ser	Ala Ser Ser Val Val Ser
575	580 585
Pro Ser Phe Val Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val Gln
590	595 600
Phe Gln Pro Asn Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu Ser
605	610 615
Asn Leu Ala Thr Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val Asn
620	625 630
Ala Ser Ala Ser Cys His Val Leu Pro	Thr Gly Asp Leu Leu Leu
635	640 645
Val Gly Thr Gln Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu Glu
650	655 660
Glu Gly Phe Gln Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val Val
665	670 675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro
680	685 690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
				695					700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
				710					715					720	
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
				725					730					735	
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
				740					745					750	
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
				755					760					765	
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
				770					775					780	
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
				785					790					795	
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
				800					805					810	
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
				815					820					825	
Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val				
				830					835						

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 254
 agcccgtagc gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 tgaagccagg gcagcgtcct ctgg 24

<210> 256
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 256
gtacaggctg cagttggc 18

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<210> 257
<211> 41
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

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<400> 257
aqaagccatg tgagcaagtc cagttccagc ccaacacagt g 41
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<210> 258
<211> 45
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

<400> 258
gagctgcaga tcttctcattc gggacagccc gtgcagaatc tgctc 45

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<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens
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<220>  
<221> unsure  
<222> 3635  
<223> unknown base
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<400> '259
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agggcgggac gggagcccg actcgtctgc cgccgccgtc gtcgccgtcg 150
tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200
cgcccgagcc gccgctagcg cgcgccgggc atgggtccct cttaaaggcg 250
caggccgcgg cggcgggggc ggggtgtgcgg aacaaagcgc cggcgcgggg 300
cctgcggggc gctcgggggc cgcgatgggc gcggcgggcc cgcggcgggc 350
gcggcgctgc ccgggcccgg cctcgcgggc ctagggcggg ctggcctccg 400
tgggcggggg cagcggggtg agggcgcgcg gagcctgcgg cggcggcggc 450
```


ggccggcgcg gggcccgcc gggcgagcg ggcggggcat ggccgcgcgc 500
 ggccggcgcg cctggctcag cgtgctgctc gggctcgtcc tgggcttcgt 550
 gctggcctcg cggtcgtcc tggccggggc ttccgagctg aagcgagcg 600
 gccacggcg ccgcgccagc cccgagggct gccgggtccg gcaggcgcg 650
 gttcccgag ccggcggggc gcgcggcgat gcgcgcgggg cgcagctctg 700
 gccggccggc tcggacccag atggcgggccc gcgcgacagg aactttctct 750
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 aagtgagggg tctgacacat ctgtaccaat tccagtagtg ccactacggg 900
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 acattggcaa gtgtctccgg gagatgtaca ccacccatga ggacgtggag 1250
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 aagtggtttt cttacatagg actcctttaa gattgagctt tctgaacaag 3050
 aaggatgaca gtgtttgcct ttgaacacat cttcttgctg aacattatgt 3100
 agcagacctg cttactttg acttgaaatg tacctgatga acaaaacttt 3150
 tttaaaaaaa tgttttcttt tgagacctt tgctccagtc ctatggcaga 3200
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<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	20	25	30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	35	40	45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	50	55	60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	65	70	75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	80	85	90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	95	100	105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	110	115	120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	125	130	135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	140	145	150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	155	160	165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	170	175	180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	185	190	195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	200	205	210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	215	220	225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	230	235	240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	245	250	255	
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	260	265	270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys				

	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln	Ala
	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg	Leu
	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His	Arg
	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr	Ser
	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro	Pro
	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu	Glu
	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp	Gly
	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala	Leu
	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn	Ala
	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr	Gly
	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu	Asp
	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr	Val
	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys	Ile
	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala	Lys
	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn	Ser
	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser	Glu
	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro	Leu
	530	535	540
Ser Gly Arg Phe	Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu
	545	550	555
Lys Thr Cys Leu	Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu

				560					565					570
Leu	Phe	Asn	Ser	Asp 575	Ser	Asn	Pro	Asp	Lys 580	Ala	Lys	Gln	Val	Glu 585
Leu	Met	Arg	Asp	Tyr 590	Arg	Ile	Lys	Tyr	Pro 595	Lys	Ala	Asp	Met	Gln 600
Ile	Leu	Pro	Val	Ser 605	Gly	Glu	Phe	Ser	Arg 610	Ala	Leu	Ala	Leu	Glu 615
Val	Gly	Ser	Ser	Gln 620	Phe	Asn	Asn	Glu	Ser 625	Leu	Leu	Phe	Phe	Cys 630
Asp	Val	Asp	Leu	Val 635	Phe	Thr	Thr	Glu	Phe 640	Leu	Gln	Arg	Cys	Arg 645
Ala	Asn	Thr	Val	Leu 650	Gly	Gln	Gln	Ile	Tyr 655	Phe	Pro	Ile	Ile	Phe 660
Ser	Gln	Tyr	Asp	Pro 665	Lys	Ile	Val	Tyr	Ser 670	Gly	Lys	Val	Pro	Ser 675
Asp	Asn	His	Phe	Ala 680	Phe	Thr	Gln	Lys	Thr 685	Gly	Phe	Trp	Arg	Asn 690
Tyr	Gly	Phe	Gly	Ile 695	Thr	Cys	Ile	Tyr	Lys 700	Gly	Asp	Leu	Val	Arg 705
Val	Gly	Gly	Phe	Asp 710	Val	Ser	Ile	Gln	Gly 715	Trp	Gly	Leu	Glu	Asp 720
Val	Asp	Leu	Phe	Asn 725	Lys	Val	Val	Gln	Ala 730	Gly	Leu	Lys	Thr	Phe 735
Arg	Ser	Gln	Glu	Val 740	Gly	Val	Val	His	Val 745	His	His	Pro	Val	Phe 750
Cys	Asp	Pro	Asn	Leu 755	Asp	Pro	Lys	Gln	Tyr 760	Lys	Met	Cys	Leu	Gly 765
Ser	Lys	Ala	Ser	Thr 770	Tyr	Gly	Ser	Thr	Gln 775	Gln	Leu	Ala	Glu	Met 780
Trp	Leu	Glu	Lys	Asn 785	Asp	Pro	Ser	Tyr	Ser 790	Lys	Ser	Ser	Asn	Asn 795
Asn	Gly	Ser	Val	Arg 800	Thr	Ala								

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 263
ccagaagaag tccttcacga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtag gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400
tgttttaacc aatcctatca gtgaagaaac tacaacttcc cctacaggag 450
gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccocatc 500
tggtcgatca aaccaaaca tgtttccatt gttttgcatg cagaggaacc 550
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[illegible]

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<210> 265
<211> 350
<212> PRT
<213> Homo sapiens
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Ser  Val  Pro  Ala  Tyr  Pro  Ser  Ile  Thr  Val  Thr  Pro  Asp  Glu  Glu
          20          25          30
Gln  Asn  Leu  Asn  His  Tyr  Ile  Gln  Val  Leu  Glu  Asn  Leu  Val  Arg
          35          40          45
Ser  Val  Pro  Ser  Gly  Glu  Pro  Gly  Arg  Glu  Lys  Lys  Ser  Asn  Ser
          50          55          60
Pro  Lys  His  Val  Tyr  Ser  Ile  Ala  Ser  Lys  Gly  Ser  Lys  Phe  Lys
          65          70          75
Glu  Leu  Val  Thr  His  Gly  Asp  Ala  Ser  Thr  Glu  Asn  Asp  Val  Leu
          80          85          90

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<210>	266
<211>	2403
<212>	DNA

<210>	266
<211>	2403
<212>	DNA

<213> Homo sapiens

<400> 266

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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
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gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250
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caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact 350
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 caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
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 aaa 2403

<210> 267
 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 267
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 20 25 30
 Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

				35					40					45
Thr	Ser	Ala	Glu	Ala 50	Met	Glu	Val	Arg	Phe 55	Phe	Arg	Asn	Gln	Phe 60
His	Ala	Val	Val	His 65	Leu	Tyr	Arg	Asp	Gly 70	Glu	Asp	Trp	Glu	Ser 75
Lys	Gln	Met	Pro	Gln 80	Tyr	Arg	Gly	Arg	Thr 85	Glu	Phe	Val	Lys	Asp 90
Ser	Ile	Ala	Gly	Gly 95	Arg	Val	Ser	Leu	Arg 100	Leu	Lys	Asn	Ile	Thr 105
Pro	Ser	Asp	Ile	Gly 110	Leu	Tyr	Gly	Cys	Trp 115	Phe	Ser	Ser	Gln	Ile 120
Tyr	Asp	Glu	Glu	Ala 125	Thr	Trp	Glu	Leu	Arg 130	Val	Ala	Ala	Leu	Gly 135
Ser	Leu	Pro	Leu	Ile 140	Ser	Ile	Val	Gly	Tyr 145	Val	Asp	Gly	Gly	Ile 150
Gln	Leu	Leu	Cys	Leu 155	Ser	Ser	Gly	Trp	Phe 160	Pro	Gln	Pro	Thr	Ala 165
Lys	Trp	Lys	Gly	Pro 170	Gln	Gly	Gln	Asp	Leu 175	Ser	Ser	Asp	Ser	Arg 180
Ala	Asn	Ala	Asp	Gly 185	Tyr	Ser	Leu	Tyr	Asp 190	Val	Glu	Ile	Ser	Ile 195
Ile	Val	Gln	Glu	Asn 200	Ala	Gly	Ser	Ile	Leu 205	Cys	Ser	Ile	His	Leu 210
Ala	Glu	Gln	Ser	His 215	Glu	Val	Glu	Ser	Lys 220	Val	Leu	Ile	Gly	Glu 225
Thr	Phe	Phe	Gln	Pro 230	Ser	Pro	Trp	Arg	Leu 235	Ala	Ser	Ile	Leu	Leu 240
Gly	Leu	Leu	Cys	Gly 245	Ala	Leu	Cys	Gly	Val 250	Val	Met	Gly	Met	Ile 255
Ile	Val	Phe	Phe	Lys 260	Ser	Lys	Gly	Lys	Ile 265	Gln	Ala	Glu	Leu	Asp 270
Trp	Arg	Arg	Lys	His 275	Gly	Gln	Ala	Glu	Leu 280	Arg	Asp	Ala	Arg	Lys 285
His	Ala	Val	Glu	Val 290	Thr	Leu	Asp	Pro	Glu 295	Thr	Ala	His	Pro	Lys 300
Leu	Cys	Val	Ser	Asp 305	Leu	Lys	Thr	Val	Thr 310	His	Arg	Lys	Ala	Pro 315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val

SECRET

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<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens
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gtcatcttca tatccctgat tgcctggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgttg ctcatatgct gttgatttgt 400
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tgttttacat gaaaagctgc aagatgctgt aggacccctt aaagtagatc 500
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ctcactcagtg taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtgct 600
caggatcgtt ggtgggacag aagtagaaga gggatgaatgg ccttggcagg 650
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catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
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Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
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Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
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Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
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Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
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Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
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Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
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<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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 <213> Homo sapiens

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 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
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 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
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 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
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<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
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His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
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Asp	Gln	Trp	His	395	Val	Val	Gly	Ile	400	Val	Ser	Trp	Gly	Tyr	Gly	405
Gly	Gly	Pro	Ser	410	Thr	Pro	Gly	Val	415	Tyr	Thr	Lys	Val	Ser	Ala	420
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<210> 276
<211> 3143
<212> DNA
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<400> 276

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<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
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Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
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230		235 240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe Asp
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Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys Lys
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275		280 285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu Pro
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Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val
320		325 330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335		340 345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
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Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365		370 375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380		385 390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr
395		400 405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410		415 420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425		430 435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440		445 450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455		460 465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470		475 480

Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala	485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg	500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu	515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg	530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser	545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala	560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala	575	580	585
Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu	590	595	600
Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln	605	610	615
Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly	620	625	630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln	635	640	645
Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His	650	655	660
Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala	665	670	675
Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu	680	685	690
Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser	695	700	705
Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu	710	715	720
Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His	725	730	735
Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp	740	745	750
Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala	755	760	

<210> 278
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 278
ctgctgggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctgtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
catcttgatca tgtacctggg aaccaccaca gggctgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

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ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
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<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile

155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu	Phe Gly Leu Pro Ile Pro	
170	175	180
Leu Ser Tyr Val Pro Val Phe Arg Ser	Leu Leu Thr Asp His Met	
185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe	Leu Met Phe Phe Ser Phe	
200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser	Thr Phe Asp Asn Thr Ile	
215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg	Pro Val Leu Ser His Leu	
230	235	240
Leu Leu Lys Ala Glu Leu Trp Phe Ile	Asn Ser Asp Phe Ala Phe	
245	250	255
Asp Phe Ala Arg Pro Leu Leu Pro Asn	Thr Val Tyr Val Gly Gly	
260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	

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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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				20				25						30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35				40						45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50				55						60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65				70						75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
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Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
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<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

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<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290

ctgtgctact gcccttgga cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

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<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292
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 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180

[illegible]

<223> Synthetic oligonucleotide probe

cccacagaca cccatgacac ttcc 24

<211> 50

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

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<211> 3060

<213> Homo sapiens

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 catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150
 ggggtcaggc tgatctcaaa ctctgagtt caggtgatct gccgcctca 2200
 gcctccaaa gtgttgatg tgcaggcgtg agccactgcg cctggccgga 2250

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 ttgttctgtt gccagggctg gagtacagtg gcacagtctt ggctcactgc 2650
 agcctcgacc tcctgggctg cagtgatcct cccacctcag cctcccttgt 2700
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 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacta 2950
 ccaggagac tgaagtggga ggatcgcttg gccatgagaa gtcgaggctg 3000
 cagtgaagtc aggttgtgcg actgcattcc agcctggaca acagagtga 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
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 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
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 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

(The following information was obtained from the above-mentioned sources.)

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu		Ile	Asp	Phe	Leu	Cys	Gly				
				95						100					105				
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val		Leu	Gly	Ser	Ser	Lys	Val				
				110						115					120				
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val		Pro	Leu	Ile	Gly	Trp	Thr				
				125						130					135				
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys		Lys	Arg	Lys	Trp	Glu	Glu				
				140						145					150				
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu		Arg	Arg	Leu	Ser	Asp	Tyr				
				155						160					165				
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr		Cys	Glu	Gly	Thr	Arg	Phe				
				170						175					180				
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met		Glu	Val	Ala	Ala	Ala	Lys				
				185						190					195				
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu		Leu	Pro	Arg	Thr	Lys	Gly				
				200						205					210				
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg		Gly	Thr	Val	Ala	Ala	Val				
				215						220					225				
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly		Asn	Lys	Asn	Pro	Ser	Leu				
				230						235					240				
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr		Glu	Ala	Asp	Met	Cys	Val				
				245						250					255				
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro		Leu	Asp	Glu	Lys	Glu	Ala				
				260						265					270				
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln		Glu	Lys	Asp	Ala	Leu	Gln				
				275						280					285				
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe		Pro	Gly	Glu	Gln	Phe	Lys				
				290						295					300				
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu		Asn	Phe	Leu	Ser	Trp	Ala				
				305						310					315				
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser		Phe	Val	Leu	Gly	Val	Phe				
				320						325					330				
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu		Thr	Phe	Leu	Gly	Phe	Val				
				335						340					345				
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg		Leu	Ile	Gly	Glu	Ser	Leu				
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<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
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<210> 299
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gccacctcca tgctaacgcg g 21

<210> 300
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 300
ccaaggtcct cgctaagaag gagctgctct acgtgcccct catcg 45

<210> 301
<211> 1334
<212> DNA
<213> Homo sapiens

<400> 301
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tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150
tcagtttgtc ttgtgggggt ggtggcaggc aggccggcct acgcctgata 200
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
tagctggggg ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
 tgtcgttctt gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
 ctggcctgac agaatctcat cttgtttaat gctctcataa gaccacttgt 650
 ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
 gttgtatggg ttgtgtctgt tccccagaat gccagctct gagctgctg 750
 agggatcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg ccagcattg taaattcaca 900
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 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagtggag actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302
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 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
 20 25 30
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
 35 40 45
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
 50 55 60
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp

	65		70		75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr					
	80		85		90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln					
	95		100		105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu					
	110		115		120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr					
	125		130		135
Cys Gly Val Leu Leu Ser Phe Leu					
	140				

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
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 ggcgatggct cccactgccc aggcacagc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggccc gtggacacct gctcagaagc agtgggtgag 600
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 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
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 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

[illegible][illegible]

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<210> 305
<211> 989
<212> DNA
<213> Homo sapiens
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<400> 305
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ccggctctcc gtgcccgcgc cgctggccctt gggctcagcc gcaactgggcg 150
ccgccttcgc cactggcctc ttctgtggga ggcggtgccc cccatggcga 200
ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250
gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300
ggctgctgac cctggagcag ccgcagggggg attctatgat gacctgcgag 350
caggcccagc tcttggccaa cctggcgcgcg ctcatccagg ccaagaaggc 400
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[illegible]

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				20					25					30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys	
				35					40					45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser	
				50					55					60	
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				65					70					75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
				80					85					90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
				95					100					105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
				110					115					120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
				245					250					255	

(The following information was obtained from the records of the Federal Bureau of Investigation, Department of Justice.)

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<210> 308
<211> 671
<212> PRT
<213> Homo sapiens
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<400> 308
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Lys  Gly  Tyr  Pro  His  Trp  Pro  Ala  Arg  Ile  Asp  Asp  Ile  Ala  Asp
          20          25          30

Gly  Ala  Val  Lys  Pro  Pro  Pro  Asn  Lys  Tyr  Pro  Ile  Phe  Phe  Phe

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35										40					45				
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro					
				50					55					60					
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys					
				65					70					75					
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala					
				80					85					90					
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala					
				95					100					105					
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp					
				110					115					120					
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala					
				125					130					135					
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser					
				140					145					150					
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
				155					160					165					
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
				170					175					180					
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
				185					190					195					
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
				200					205					210					
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
				215					220					225					
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
				230					235					240					
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
				245					250					255					
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
				260					265					270					
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
				275					280					285					
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
				290					295					300					
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
				305					310					315					
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg					

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605	610	615
Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg		
620	625	630
Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro		
635	640	645
Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala		
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Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser		
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<210> 309
 <211> 3871
 <212> DNA
 <213> Homo sapiens

<400> 309
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 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200
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 aaaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450
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 ggagcatttc atccaatatg tgggtatatt gatcttggag tctacaagga 600
 ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650
 aatgtccttt cgatcctcag cagccttttg cttcagtaat gacagatgag 700
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 cactcgatcc cttgggccta ctcatgacca ccactacatc agaactgaca 800
 tttcagagca ctactggctc aatggagcaa aatttattgg aactttcttc 850
 ataccagaca cctacaatcc agatgatgat aaaatatatt tcttctttcg 900
 tgaatcatct caagaaggca gtacctccga taaaaccatc ctttctcgag 950

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 aagtggacga cttttcttaa ggccagactg atttgctcaa ttcttggaag 1050
 tgatggggca gatacttact ttgatgagct tcaagatatt tatttactcc 1100
 ccacaagaga tgaaagaaat cctgtagtat atggagtctt tactacaacc 1150
 agtccatct tcaaaggctc tgctgtttgt gtgtatagca tggctgacat 1200
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 gttgggtgca gtatgatggg agaattcctt atccacggcc tggtagatgt 1300
 ccaagcaaaa cctatgaccc actgattaag tccacccgag attttccaga 1350
 tgatgtcatc agtttcataa agcggcactc tgtgatgtat aagtccgtat 1400
 acccagttgc aggaggacca acgttcaaga gaatcaatgt ggattacaga 1450
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 agcatcgaga ggagttgaag cccgatgaaa gaatcatcaa aacggaatat 2050
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 caaagcccag gagcacactt tcatccacac catagtgaag ctgactttga 2150
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Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp		
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<212> PRT

<213> Homo sapiens

<400> 315

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Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser
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Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu
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Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
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Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
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Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
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Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
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Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
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Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
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Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
290 295 300

Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala
305 310 315

Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly
320 325 330

Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro
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<211> 1197

<212> DNA

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Ala	Pro	Pro	Arg	Ala 200	Thr	Thr	Thr	Thr	Ala 205	Asn	Thr	Ala	Pro	Ala 210	
Tyr	Gln	Pro	Pro	Ala 215	Ala	Tyr	Lys	Asp	Asn 220	Arg	Ala	Pro	Ser	Val 225	
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<210> 325
<211> 2121
<212> DNA
<213> Homo sapiens
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cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
gcacgcgcgc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
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aaccccgctca	cctccgtggt	ccagtagcgaa	gggctctgga	ggagctgcgt	250
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gacttccagc	catgctgcag	gcagtgcgag	ccctgatgat	cgtaggcata	350
gtcctgggtg	ccattggcct	cctggtatcc	atctttgccc	tgaaatgcat	400
ccgcattggc	agcatggagg	actctgccaa	agccaacatg	acactgacct	450
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caactacaaa	gccgtttctt	atcatgcctc	aggccacagt	gttgcttaca	750
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ggaagaaact	cccggagagc	tcacccaaaa	aacaaggaga	tcccatctag	950
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 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
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<210> 327
<211> 2010
<212> DNA
<213> Homo sapiens
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gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
cattgaaaac aacatcgtgg tttttgaaaa ctctctgggaa ggactgtgga 250
tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
tccctgctgg ctcttttctcc ggacctacag gcagccagag gactgatgtg 350
tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca 400
tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tggtgctcat 500
ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
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tggaaccagg cactgggtgt gattgttgga ggagctctgt tctgctgcgt 650
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 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaattctt aattacagga 900
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taagggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattatct tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgt acatttatat ctccataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaagggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcttc catttataat 1300
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 gagtacagac ttgaggttt catcaatata aataaaagag cagaaaaata 1700
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 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

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1 5 10 15

Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
35 40 45

Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
65 70 75

Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
95 100 105

Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
125 130 135

Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
155 160 165

Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
185 190 195

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<400> 329
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<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
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Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
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<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50		55		60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65		70		75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80		85		90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95		100		105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110		115		120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125		130		135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140		145		150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155		160		165
Ser Lys Thr Ser Thr Ser Tyr Val	170				

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
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aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatccc aggtctctgac tgagtttctt tcagttttac tgatgttctg 400
gggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450
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<210> 335
<211> 742
<212> DNA
<213> Homo sapiens
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tggccctgac cgggctggcg ctgctcctgc tcctgtgtg gggcccaggt 150
ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200
tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
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agcgattctc ttcattgtat tcctaattgcc ttacactact tggtttctga 600
tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaattgctt tttgatattt catgggaatg 700

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<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
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Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgtc agggaccca acgcatccc agccagcgc 250
agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
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 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctccaa ctgcgttctc cactgccacg 600
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 acgccaggtc ggtgggagc tgggaaggg gagcggggag gggcagagga 1250
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<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
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 20 25 30
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 35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
50 55 60

Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
65 70 75

His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
80 85 90

Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
95 100 105

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
110 115 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
125 130 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
140 145 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
155 160 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
170 175 180

Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
185 190 195

Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
200 205 210

Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
215 220 225

Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
230 235 240

Phe Ala Met Tyr Arg Pro
245

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

100-443887-1000

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

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Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
 140 145

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 341
 ccctccaagg atgacaaagg cgc 23

<210> 342
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 342
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 343
 atctcaggcg gcatcctgtc agcc 24

<210> 344
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 344
 gtggatgcct gcaagaaggt tggg 24

<210> 345
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 345

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<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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<212> PRT

<213> Homo sapiens

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Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	35	40	45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	50	55	60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	65	70	75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	80	85	90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	95	100	105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	110	115	120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	125	130	135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	140	145	150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	155	160	165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	170	175	180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	185	190	195	
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Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	215	220	225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	230	235	240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	245	250	255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	260	265	270	

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Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
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<213> Homo sapiens

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<400> 356
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 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln

1. The first part of the document is a list of references. The references are listed in a standard format, with the author's name, the title of the work, and the publisher. The references are as follows:

1. J. H. Van Veen, *The History of the Netherlands*, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579,

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
1 5 10 15

Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
20 25 30

Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
35 40 45

Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
50 55 60

Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
65 70 75

His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
80 85 90

Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
95 100 105

Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
110 115 120

Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
125 130 135

Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
140 145 150

Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
155 160 165

Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180

Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
ccagcagtgc ccatactcca tagc 24

<210> 360
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
tgacgagtgg gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gctctacgga aacttctgct gtgg 24

<210> 362
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 362
 attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
 <211> 1777
 <212> DNA
 <213> Homo sapiens

<400> 363
 ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
 ccggcgcggg tggcggagag atcagaagcc tcttcccaaa gccgagccaa 100
 cctcagcggg gacccgggct cagggacgcg gcggcgggcg cggcgactgc 150
 agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
 cccagacagc cggcgtggc tgtggtcggt gctggcgggc gcgcttgggc 250
 tcttgacagc tggagtatca gccttgaag tatatacgcc aaaagaaatc 300
 ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
 tagtacgact ggcggggtga cctcagtctc ctggagcttc cagccagagg 400
 gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
 cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
 tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatatacaca 550
 atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
 cctggacaca ttaggtctta tgtcgtagaa aaagagaatt tgctgtgtt 650
 tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700
 ctctgtcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
 aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
 gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
 tgccttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900
 tccggcgagc atcacagtga caagattaac aagtcagagt ctgtggtgta 950
 tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
185 190 195

Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
200 205 210

Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
215 220 225

Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
230 235 240

Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
245 250 255

Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
260 265

<210> 365
<211> 1321
<212> DNA
<213> Homo sapiens

<400> 365
gccggctgtg cagagacgcc atgtaccggc tctgtgcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccg 300
agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccggggcat 400

agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500
 cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaaggtttc tgtcacaaca 650
 agattactga tttcccattht aagtgggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaagge gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
 gatcctttgt tottcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactattht tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5				10						15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20				25						30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35				40						45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50				55						60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagaa gtctggtcag aaggtttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttggtt cattctctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccgggcc gggactgggt gcgagggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
tgggacactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
tactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctgggt gctatgtctc ctcccttgtc cctgcgtgct ccctgggtga 500
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tgggtggcgt gtcggtgggt acgcaccccg ggggctgccg gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgccctg 700
agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtcgtcctgt tctcatgat 800
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaaacc 1050
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaaa 1150

<210> 372
<211> 269
<212> PRT
<213> Homo sapiens

<400> 372
Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu
1 5 10 15
Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggaaacccga gccggagccg gagccacagc ggggaggggtg 50
 gcttgccggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

[illegible]

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<210> 374
<211> 450
<212> PRT
<213> Homo sapiens
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<400> 374															
Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	
1				5					10					15	
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	
				20					25					30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	
				35					40					45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	
				50					55					60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	
				65					70					75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	
				80					85					90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	
				95					100					105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	
				110					115					120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	
				125					130					135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	
				140					145					150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	
				155					160					165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	
				170					175					180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	
				185					190					195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	
				200					205					210	

gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcgg ccacaggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaaagg actttgggtg tatctttcac acaaggtatg agcagattca 250
 ccttgteccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtg agagggggg ctgctccttc 350
 ctctccaaga ctcggttggg ccaggagcac ggcgggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
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 gacggctaca tgatccgcg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
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 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900
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 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
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<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10					15	

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25					30	

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40					45	

1. The first group of people who are interested in the results of the study are the researchers themselves. They want to know if the study was successful in achieving its objectives and if the data collected is reliable and valid. They also want to know if the study has contributed to the existing knowledge in the field and if it has any practical implications.

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 381
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382
 <211> 764
 <212> DNA
 <213> Homo sapiens

<400> 382
 ctgcgttctt ccttctggat gggggcccag gggggcccagg agagtataaa 50
 ggcgatgtgg aggggtgccg gcacaaccag acgcccagtc acaggcgaga 100
 gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
 ctectggggg gccccacctg ggcaggggaag atgtatggcc ctggaggagg 200
 caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
 ggggtgtctgt aggtcttctc ctgggtgaaaa gtgtccaggt gaaacttgga 300
 gactcctggg acgtgaaaact gggagcctta ggtgggaata cccaggaagt 350
 caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
 ctttctctccg gggatgggtc atgtacacca gcaaggaccg ctatttctat 450
 tttgggaagc ttgatggcca gatctcctct gcctacocca gccagagggg 500
 gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatacaaga 550
 gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
 ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650
 ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700
 actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
 gcttctgcag aaaa 764

<210> 383
 <211> 178
 <212> PRT
 <213> Homo sapiens

<400> 383
 Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
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Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60

Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75

Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90

Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105

Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120

Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135

Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
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Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
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Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

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atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttcctggg 400
tgtcagcgag ccctgactca ctacagtga gctgacaggg gctgtcatgc 450

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cactggttat	agccccact	gtcttactga	caatgctttc	ttctgccgaa	600
cgaggatgcc	ctaagggctg	taggtgtgaa	ggcaaaatgg	tatattgtga	650
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gtttgtccct	tcgctataac	agccttcaaa	aacttaagta	taatcaattt	750
aaagggctca	accagctcac	ctggctatac	cttgaccata	accatatcag	800
caatattgac	gaaaatgctt	ttaatggaat	acgcagactc	aaagagctga	850
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Glu Gln Phe Arg Gly Leu Arg Lys Leu	155	Leu Ser Leu His Leu Arg	160	165
Ser Asn Ser Leu Arg Thr Ile Pro Val	170	Arg Ile Phe Gln Asp Cys	175	180
Arg Asn Leu Glu Leu Leu Asp Leu Gly	185	Tyr Asn Arg Ile Arg Ser	190	195
Leu Ala Arg Asn Val Phe Ala Gly Met	200	Ile Arg Leu Lys Glu Leu	205	210
His Leu Glu His Asn Gln Phe Ser Lys	215	Leu Asn Leu Ala Leu Phe	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu	230	Tyr Leu Gln Trp Asn Lys	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser	245	Trp Thr Trp Ser Ser Leu	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu	260	Ile Glu Ala Phe Ser Gly	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn	275	Leu Gln Arg Leu Asn Leu	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly	290	Gln Glu Ile Leu Asp Ser	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu	305	Ala Gly Asn Ile Trp Glu	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val	320	Asn Trp Leu Lys Ser Phe	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile	335	Cys Ala Ser Pro Lys Glu	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala	350	Val Lys Asn Tyr Ser Ile	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe	365	Asp Leu Ala Arg Ala Leu	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu	380	Pro Arg Pro Lys His Glu	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val	395	Gly Ala Thr Glu Pro Gly	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His	410	Ile Ser Phe His Lys Ile	415	420
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SECRET

[illegible]

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Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
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Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
          35          40          45

His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
          50          55          60

Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
          65          70          75

Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
          80          85          90

Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
          95          100          105

Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
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<400> 392

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<210> 393

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<212> DNA

<213> Homo sapiens

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Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp	
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Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala	
				140					145					150	
Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser	
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His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly	
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Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg	
				185					190					195	
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu	
				200					205					210	
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe	
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Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln	
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Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly	
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Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala	
				260					265					270	
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp	
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Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu	
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His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg	
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Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	
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Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser	
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

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Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60

Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75

Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
95 100 105

Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
110 115 120

Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
125 130 135

Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
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Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
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Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
170 175 180

Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
185 190 195

Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
200 205 210

Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
215 220 225

Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
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Trp Met Glu Glu Thr Glu
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<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

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Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
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Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
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Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
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Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
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Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
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Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
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Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
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Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
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Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg
 305 310 315

Glu Met Ser Gly Val Ser Pro Phe
 320

<210> 407
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 407
 cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 408
 gcggaattct taaaatggac tgactccact catc 34

<210> 409
 <211> 1487
 <212> DNA
 <213> Homo sapiens

<400> 409
 cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
 tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
 cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150
 tagataatth tcgttgccca gaatgtgaat gtattgactg gagtgaagaga 200
 agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
 gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
 accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcattg 350

(The following information was obtained from the above-mentioned sources.)

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<210> 414
<211> 1337
<212> DNA
<213> Homo sapiens
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<400> 414
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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtgggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atcgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgccagacc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtggggcc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaatc cggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttcggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagcccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc ccgaagcca ttttaggggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgctt ggaaggtgct 1100
gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaacct 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200

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accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
<211> 224
<212> PRT
<213> Homo sapiens

<400> 415
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1 5 10 15
Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
20 25 30
Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
35 40 45
Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
50 55 60
Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
65 70 75
Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
80 85 90
Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
95 100 105
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
110 115 120
Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
125 130 135
Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
140 145 150
Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
155 160 165
Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
170 175 180
Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
185 190 195
Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
200 205 210
Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
215 220

<400>	422				
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tgtcctgggg	atccagaaac	ccatgatacc	ctactgaaca	ccgaatcccc	100
tggaagccca	cagagacaga	gacagcaaga	gaagcagaga	taaatacact	150
cacgccagga	gctcgctcgc	tctctctctc	tctctctcac	tcctccctcc	200
ctctctctct	gcctgtccta	gtcctctagt	cctcaaattc	ccagtcccct	250
gcaccccttc	ctgggacact	atgttgttct	ccgccctcct	gctggagggtg	300
atttgatcc	tggctgcaga	tgggggtcaa	cactggacgt	atgagggcc	350
acatggtcag	gaccattggc	cagcctctta	ccctgagtgt	ggaaacaatg	400
cccagtcgcc	catcgatatt	cagacagaca	gtgtgacatt	tgaccctgat	450
ttgcctgctc	tgcagcccca	cggatatgac	cagcctggca	ccgagccttt	500
ggacctgcac	aacaatggcc	acacagtgca	actctctctg	ccctctaccc	550
tgtatctggg	tggacttccc	cgaaaatatg	tagctgcccc	gctccacctg	600
cactgggggtc	agaaaggatc	cccagggggg	tcagaacacc	agatcaacag	650
tgaagccaca	tttgcagagc	tccacattgt	acattatgac	tctgattcct	700
atgacagctt	gagtgaggct	gctgagaggc	ctcagggcct	ggctgtcctg	750
ggcatcctaa	ttgaggtggg	tgagactaag	aatatagctt	atgaacacat	800
tctgagtcac	ttgcatgaag	tcaggcataa	agatcagaag	acctcagtgc	850
ctcccttcaa	cctaagagag	ctgctcccca	aacagctggg	gcagtaacttc	900

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala	
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly	
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His	
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu Ala	
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu	
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His	
170	175	180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro	
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe	
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln	
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro	
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn	
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr	
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly	
290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile	
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser	
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aattttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150
aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactgggggcc agatctgcat ctgttaaate 300

	95		100		105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu	Ser Ser Glu Glu Leu	Pro		
	110	115	120		
Gln Ile Phe Thr	Ser Leu Ile Ile His	Ser Leu Phe Pro Gly	Gly		
	125	130	135		
Ile Leu Pro Thr	Ser Gln Ala Gly Ala	Asn Pro Asp Val Gln	Asp		
	140	145	150		
Gly Ser Leu Pro	Ala Gly Gly Ala Gly	Val Asn Pro Ala Thr	Gln		
	155	160	165		
Gly Thr Pro Ala	Gly Arg Leu Pro Thr	Pro Ser Gly Thr Asp	Asp		
	170	175	180		
Asp Phe Ala Val	Thr Thr Pro Ala Gly	Ile Gln Arg Ser Thr	His		
	185	190	195		
Ala Ile Glu Glu	Ala Thr Thr Glu Ser	Ala Asn Gly Ile Gln			
	200	205			

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

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 cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
 ccgctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgcgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgtc gagcgccctct gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650
 attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 432
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 432
aggacttgcc ctcaggaa 18

<210> 433
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 433
cgcaggacag ttgtgaaaat a 21

<210> 434
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
atgacgctcg tccaaggcca c 21

<210> 435
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cccacctgta ccaccatgt 19

 <210> 436
 <211> 24
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 actccaggca ccactgttc tccc 24

 <210> 437
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 <400> 437
 aagggctggc attcaagtc 19

 <210> 438
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 <220>
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 <400> 438
 tgacctggca aaggaagaa 19

 <210> 439
 <211> 21
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 <220>
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 <400> 439
 cagccaccct ccagtccaag g 21

 <210> 440
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<400> 445
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<211> 22
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

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<400> 446
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<210> 447
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<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

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<400> 447
caggactgag cgcttgttta 20
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<211> 21
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

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<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

<400> 449
ccagacctca gccaggaa 18

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<210> 450
<211> 18
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<223> Synthetic oligonucleotide probe

<400> 450

ccctagctga ccccttca 18

<210> 451

<211> 23

<212> DNA

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<210> 452

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<210> 453

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<210> 454

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<212> DNA

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<400> 454

ccatgcctgc tcagccaaga a 21

<210> 455

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<223> Synthetic oligonucleotide probe

<400> 455
caggaaatct ggaaacctac agt 23

<210> 456
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<400> 456
ccttgaaaag gacccagttt 20

<210> 457
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<213> Artificial Sequence

<220>
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<400> 457
atgagtcgca cctgctgttc cc 22

<210> 458
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<213> Artificial Sequence

<220>
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<400> 458
tagcagctgc ccttggtta 18

<210> 459
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<220>
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<400> 459
aacagcaggt gcgactcatc ta 22

<210> 460
<211> 23
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 460
tgctaggcga cgacacccag acc 23

<210> 461
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
tggacacgtg gcagtgga 18

<210> 462
<211> 19
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 462
tcatggtctc gtcccatc 19

<210> 463
<211> 27
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<220>
<223> Synthetic oligonucleotide probe

<400> 463
caccatttgt ttctctgtct ccccatc 27

<210> 464
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<220>
<223> Synthetic oligonucleotide probe

<400> 464
ccggcatcct tggagtag 18

<210> 465
<211> 20
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 465
tccccattag cacaggagta 20

<210> 466

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 466
aggctcttgc ctgtcctgct gct 23

<210> 467
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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gcccagagtc ccaattgt 18

<210> 468
<211> 19
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<400> 468
actgctccgc ctactacga 19

<210> 469
<211> 20
<212> DNA
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<220>
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<400> 469
aggcatcctc gccgtcctca 20

<210> 470
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<212> DNA
<213> Artificial Sequence

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<400> 470
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<210> 471
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<213> Artificial Sequence

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cgagtgtgtg cgaaacctaa 20

<210> 472

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472

tcagggtcta catcagcctc ctgc 24

<210> 473

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

aaggccaagg tgagtccat 19

<210> 474

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

cctactgagg agccctatgc 20

<210> 475

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

tccaggtgga cccacttca gg 22

<210> 476

<211> 24

<212> DNA

<213> Artificial Sequence

[illegible]

<400> 476

<210> 477

<212> DNA

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

-230-

-1-